

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:38:30 ; Search time 2211 Seconds

(without alignments)
10609.164 Million cell updates/sec

Title: us-09-966-881-13

Perfect score: 806 1 TGTTCCTCCTTCGATCACA.....TCCCTTCCTCATGATNG 806

Sequence: 1 TGTTCCTCCTTCGATCACA.....TCCCTTCCTCATGATNG 806

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 45 summaries

GenBank:*

1: gb_da:*

2: gb_hlg:*

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5: gb_ov:*

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40: em_higo_mus:*

41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	96.5	806	6 A70152	A70152 Sequence 13
2	612.4	76.0	1788	6 AF206320	AF206320 Musa acum
3	591.8	73.4	748	6 A83011	A83011 Sequence 18
4	591.2	73.3	745	6 A83004	A83004 Sequence 11
5	588.8	73.1	793	6 A83001	A83001 Sequence 8
6	588.8	73.1	793	6 MA299965	299965 Musa acum
7	572.2	71.0	727	6 A83014	A83014 Sequence 21
8	543.8	67.5	727	6 A70155	A70155 Sequence 16
9	536	66.5	724	6 A70157	A70157 Sequence 18
10	510.8	63.4	704	6 A83000	A83000 Sequence 7
11	496.8	61.6	706	6 A83012	A83012 Sequence 19
12	174.4	21.6	127202	2 OSJN00272	AL731627 Oryza sat
13	169.4	21.0	1633	8 AY085026	AY085026 Arabidops
14	152	18.9	90142	8 ATAC016827	AC016827 Arabidops
15	151	18.7	823	6 A83003	A83003 Sequence 10
16	150	18.6	1408	8 FX053550	U63550 Fragaria x
17	148	18.4	1523	8 AY086099	AY086099 Arabidops
18	144.8	18.0	1496	8 AF206319	AF206319 Musa acum
19	144.4	17.9	749	6 A82999	A82999 Sequence 6
20	143.2	17.8	1462	8 MAPFL	X92943 M.acuminata
21	142.8	17.7	842	6 A70156	A70156 Sequence 17
22	141.4	17.5	708	6 A83002	A83002 Sequence 9
23	141	17.5	1525	8 AY050404	AY050404 Arabidops
24	141	17.5	1556	8 AY050795	AY050795 Arabidops
25	134.6	16.7	687	6 A70153	A70153 Sequence 14
26	134.6	16.7	687	6 MA299977	299977 Musa acum
27	133.2	16.5	5368	8 AF339024	AF339024 Fragaria
28	131.6	16.3	772	6 A83010	A83010 Sequence 17
29	131.6	16.3	772	6 MA299970	299970 Musa acum
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37	127	15.8	1459	8 AY065034	AY065034 Arabidops
38	127	15.8	1788	8 AY054200	AY054200 Arabidops
39	126.2	15.7	731	6 A83009	A83009 Sequence 16
40	124	15.4	1440	6 AX005936	AX005936 Sequence
41	124	15.4	1440	6 ZEPCLY	Y09541 Z.elegans m
42	123.6	15.3	4143	8 AF339025	AF339025 Fragaria
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ALIGNMENTS

RESULT 1

A70152 LOCUS 806 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 13 from Patent WO9811228.

ACCESSION A70152

VERSION A70152.1 GI:4774567

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 806)

AUTHORS Seymour G.B., Bird,C.R. and Medina-Suarez,R.D.

TITLE GENETIC CONTROL OF FRUIT RIPENING

PATENT: WO 9811228-A-13 19-MAR-1998;

JOURNAL SEYMOUR GRAHAM BARRON (GB)

FEATURES
Source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-068"

BASE COUNT 157 a 229 c 212 g 180 t 28 others

ORIGIN

Query Match 96.5%; Score 778; DB 6; Length 806;
Best Local Similarity 100.0%; Pred. No. 3.8e-193;
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCAATGACGGCGGTTTAAAGATGATCTCTCTCTCTCTCTCTCTCTCTG 120
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OY 781 CCCCNCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 806
DB 781 CCCCNCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 806

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RESULT 2 AF206320 1788 bp mRNA linear PLN 21-DEC-1999
LOCUS AF206320
DEFINITION Musa acuminata pectate lyase 2 (PL2) mRNA, complete cds.

ACCESSION AF206320
VERSION AF206320.1 GI:6606533
KEYWORDS
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa.

REFERENCE 1 (bases 1 to 1788)
Ong,C.R., Pua,E.C. and Liu,P.
Molecular cloning and characterization of pectate lyase in banana
Unpublished
2 (bases 1 to 1788)
Ong,C.R., Pua,E.C. and Liu,P.
Direct Submission
Submitted (18-NOV-1999) Department of Biological Sciences, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260

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source Location/Qualifiers
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/organism="Musa acuminata"
/cultivar="Williams"
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BASE COUNT 419 a 473 c 470 g 426 t

ORIGIN

Query Match 76.0%; Score 612.4; DB 8; Length 1788;
Best Local Similarity 88.6%; Pred. No. 1e-149;
Matches 716; Conservative 0; Mismatches 82; Indels 10; Gaps 6;

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DB 61 GCAATGACGGCGGTTTAAAGATGATCTCTCTCTCTCTCTCTCTCTCTG 120
OY 75 GCAATGACGGCGGTTTAAAGATGATCTCTCTCTCTCTCTCTCTCTCTG 134
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QY 481 CGGAGCGGGAATTTGCTGCTGTGACAGACTCCGGGACNATGATCCCGTGAATCTC 540
DB 495 CGGAGCGGGAATTTGCTGCTGTGACAGACTCCGGGACNATGATCCCGTGAATCTC 552
QY 541 GCCCGGAACTTANATACCCGCTCCCAANGAATTTGGCCCTTGGGATCCCTT 600
DB 553 GCCCGGAACTTANATACCCGCTCCCAANGAATTTGGCCCTTGGGATCCCTT 608
QY 601 AAACNCAANTGGAATCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 660
DB 609 AAACNCAANTGGAATCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 667
QY 661 CGATGAGCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 720
DB 668 CGATGAGCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 726
QY 721 TCCCAACACTTCTTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 778
DB 727 TCCCAACACTTCTTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 786
QY 779 GTCGCCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 806
DB 787 GTCGCCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 814

RESULT 3
LOCUS A83011 748 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 18 from Patent WO9853085.
ACCESSION A83011
VERSION A83011.1 GI:6732491
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 748)
AUTHORS Seymour G.B. and Bird C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 18 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
source 1..748
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Best Local Similarity 91.7%; Pred. No. 2.5e-144;
Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

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DB 16 TGTTCCTCCTTGATGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 75
QY 61 GCAATGACGCGGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTTGGGCTTCG 120
DB 76 GCAATGACGCGGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTTGGGCTTCG 135
QY 121 CTGCTTTTGAACGAGAGTCCGGGGTGATTTGGAACGAGAGTCTTGGCTGAGAAAT 180
DB 136 CTGCTTTTGAACGAGAGTCCGGGGTGATTTGGAACGAGAGTCTTGGCTGAGAAAT 195
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QY 241 TCTTGGAGAGAGGCTGTAAACCCGGGAGAGAAACCCGAGTGCAGACCCCGAGAG 300
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QY 301 GTTGCTTGCAGAGGCTGATGACATTAATAACAGCAGCGCTGCGAGATCTTTGGTAT 360
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QY 421 GTCACAGAAAAAGCTGCTGACCTGGCGCATTTGGCTTTGGACGCAACGCMATANGTGC 480
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QY 481 CGGAGCGGGAATTTGCTGCTGTGACAGACTCCGGGACNATGATCCCGTGAATCTC 540
DB 495 CGGAGCGGGAATTTGCTGCTGTGACAGACTCCGGGACNATGATCCCGTGAATCTC 555
QY 541 GCCCGGAACTTANATACCCGCTCCCAANGAATTTGGCCCTTGGGATCCCTT 600
DB 553 GCCCGGAACTTANATACCCGCTCCCAANGAATTTGGCCCTTGGGATCCCTT 608
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DB 727 TCCCAACACTTCTTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 786
QY 779 GTCGCCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 806
DB 787 GTCGCCNCNGTCTGCTGACAGACTCCCGGCAAGCAAGCAAGCAAGCAAGCAAG 814

RESULT 4
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DEFINITION Sequence 11 from Patent WO9853085.
ACCESSION A83004
VERSION A83004.1 GI:6732484
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 745)
AUTHORS Seymour G.B. and Bird C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 11 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
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Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5;

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QY 61 GCAATGACGCGGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTTGGGCTTCG 120
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Oy      241 TCTTTGGAAGAGAGGCTGTAAACCCGGGAGAGAAAGCCGAGTGCAGAGACCCCGAGAG 300
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Oy      657 CNAATGAGACNCGTCTGCTGACATGCGCAATGGGCGCTGCTCAACCAAT 716
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RESULT 5
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DEFINITION      Sequence 8 from Patent WO9853085.
ACCESSION      AB3001.
VERSION      AB3001.1 GI:6732481
KEYWORDS
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 793)
AUTHORS      Seymour,G.B. and Bird,C.R.
TITLE      GENETIC CONTROL OF FRUIT RIPENING
JOURNAL      Patent: WO 9853085-A 8 26-NOV-1998;
SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
FEATURES
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Best Local Similarity 88.7%; Pred.No.1.6e-143;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
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Oy      540 CGCCGCGGAGACATTAAATACCCCGTCTCAAGAAAGTTGCCCTCTGGAGTCCCTT 599
Db      547 CGCCGCGGAGACATTAAATACCCCGTCTCAAGAAAGTTGCCCTCTGGAGTCCCTT 602
Oy      600 TAAACNCAANTGAAATCTCNCCTCANGAGAACTCTTATGAACAGCTTTAANCA 659
Db      603 TAAACNCAANTGAAATCTCNCCTCANGAGAACTCTTATGAACAGCTTTAANCA 660
Oy      660 TCGATGAGACNCGTCTCTGCTGACATGCGCAATGGGCGCTGCTCAACCAATTTT 719
Db      661 TCGATGAGACCGG-TGTACGTGTCACATGGCAAGGGCGCTGCTCAACCAATTTT 717
Oy      720 TTCCCAACNCTCTCTCTCNCCTCANGAGAACTCTTATGAACAGCTTTAANCA 777
Db      718 ATCAACCAACNCTCNCCTCANGAGAACTCTTATGAACAGCTTTAANCA 777
Oy      778 NGTCCCNCTCCCT 792
Db      778 TGTTCCTCTCATCATCATCTTTTGTCTGGAAAGCTGAGAGTGAGAGGAGCG 792

RESULT 6
MA299965      MA299965      793 bp      mRNA      linear      PLN 03-NOV-1999
DEFINITION      Musa acuminata mRNA for putative pectate lyase (type I) (clone PBAN
ACCESSION      MA299965
VERSION      299965.1 GI:6249483
KEYWORDS
SOURCE      Musa acuminata.
ORGANISM      Musa acuminata.
REFERENCE      1 (bases 1 to 793)
AUTHORS      Drury,R., Hortensteiner,S., Donison,I., Bird,C.R. and Seymour,G.B.
TITLE      Chlorophyll catabolism and gene expression in the peel of ripening
JOURNAL      Physiol. Plantarum 107, 32-38 (1999)

```

REFERENCE 2 (bases 1 to 793)
 AUTHORS Medina-Suarez, R.
 TITLE Direct Submission
 JOURNAL Submitted (17-OCT-1997) R. Medina-Suarez, Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UNITED KINGDOM

FEATURES
 source location/Qualifiers
 1..793
 /organism="Musa acuminata"
 /cultivar="Grand Nain"
 /db_xref="taxon:4641"
 /clone="DBAN EU22"
 /cell_line="X10LR"
 /tissue_type="Fruit peel"
 /note="Musa AAA group"
 <1..>793
 /product="pectate lyase (type I)"
 /note="putative"

BASE COUNT 170 a 222 c 215 g 171 t 15 others

ORIGIN

Query Match
 Best Local Similarity 73.1%; Score 588.8; DB 8; Length 793;
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;

Db 1 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 60
 8 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 67

Qy 61 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 68 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127

Db 121 CTGGTTTGAACGGAGGTCGGGGGTTGATTTGAAAGCAGAGGTCCTCTCTCTCTCTCT 180
 128 CTGGTTTGAACGGAGGTCGGGGGTTGATTTGAAAGCAGAGGTCCTCTCTCTCTCTCT 187

Qy 181 GCGGAGCATCGCGAGAGCTTGAGAGAGGCTCCGGAACGCGACGCGCGATGCT 240
 188 GCGGAGCATCGCGAGAGCTTGAGAGAGGCTCCGGAACGCGACGCGCGATGCT 247

Db 241 TCCTTGAAGAGAGGCTGTAAACCCGGGAGCAGAAACCGCAGTCGACGACCCGAGAG 300
 248 TCCTTGAAGAGAGGCTGTAAACCCGGGAGCAGAAACCGCAGTCGACGACCCGAGAG 307

Qy 301 GTTGTCTGACGGTCTGATGACCATTAATCAACAGCAGCGGCTCGACATCTCTGTTAT 360
 308 GTTGTCTGACGGTCTGATGACCATTAATCAACAGCAGCGGCTCGACATCTCTGTTAT 367

Db 361 CTGTCTGCGGTTTACGCAACCGGATGACGACTGCTGGCGGTGCGACCTGATGGCAT 420
 368 CTGTCTGCGGTTTACGCAACCGGATGACGACTGCTGGCGGTGCGACCTGATGGCAT 427

Qy 421 GTCAACAG-AAAAAGCTGCTGACTGCGGCAATTTGGTTTGAACGCAACGNTAATGG 479
 428 GTCAACGAAAAAGCTGCTGACTGCGGCAATTTGGTTTGAACGCAACGNTAATGG 487

Db 480 CCGGAGCGGGAATTTGCTGTGACAGACTCCGGGACNATGATCCCGTGATGCT 539
 488 CCGGAGCGGGAATTTGCTGTGACAGACTCCGGGACNATGATCCCGTGATGCT 546

Qy 540 CCGCGGGGAACTTAATATACCCGCTGTCANANGAAGTTGCCCTCTGGATCCCTT 599
 547 CCGCGGGGAACTTAATATACCCGCTGTCANANGAAGTTGCCCTCTGGATCCCTT 602

Db 600 TAAACNNAANTGAATCTCNCNANGAAGAACTNTATGAACAGCTTAAACNA 659
 603 TAAACNNAANTGAATCTCNCNANGAAGAACTNTATGAACAGCTTAAACNA 660

Qy 660 TCGATGACNCTGCTCTGTCACATTCGCAATGGCGCTGCTGCAATTCCT 719
 661 TCGATGACNCTGCTCTGTCACATTCGCAATGGCGCTGCTGCAATTCCT 717

Db 720 NTCCCAACNTCTTCTTCNTNGCTCCTCCT--CCCAATGCAACCCNCGGGAATTCCT 777

Db 718 ATCACCAACATCATCTGCTCAGTCACCAAAAGCAACCCACCCGAAATTCCT 777

Qy 778 NTGCCCCNCCCT 792

Db 778 TGTCTCCACTCTCT 792

RESULT 7
 A83014
 LOCUS
 DEFINITION Sequence 21 from Patent WO9853085.
 ACCESSION A83014
 VERSION A83014.1 GI:6732494
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 727)
 AUTHORS Seymour, G.B. and Bird, C.R.
 TITLE GENETIC CONTROL OF FRUIT RIPENING
 JOURNAL PATENT: WO 9853085-A 21 26-NOV-1998;
 SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)

FEATURES
 source location/Qualifiers
 1..727
 /organism="unclassified"
 /db_xref="taxon:32644"
 /clone="U-139"

BASE COUNT 144 a 199 c 202 g 157 t 25 others

ORIGIN

Query Match
 Best Local Similarity 71.0%; Score 572.2; DB 6; Length 727;
 Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

Qy 1 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 60
 16 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 75

Db 61 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 76 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135

Qy 121 CTGGTTTGAACGGAGGTCGGGGGTTGATTTGAAAGCAGAGGTCCTCTCTCTCTCTCT 180
 136 CTGGTTTGAACGGAGGTCGGGGGTTGATTTGAAAGCAGAGGTCCTCTCTCTCTCTCT 195

Db 181 GCGGAGCATCGCGAGAGCTTGAGAGAGGCTCCGGAACGCGACGCGCGATGCT 240
 196 GCGGAGCATCGCGAGAGCTTGAGAGAGGCTCCGGAACGCGACGCGCGATGCT 255

Qy 241 TCCTTGAAGAGAGGCTGTAAACCCGGGAGCAGAAACCGCAGTCGACGACCCGAGAG 300
 256 TCCTTGAAGAGAGGCTGTAAACCCGGGAGCAGAAACCGCAGTCGACGACCCGAGAG 315

Db 301 GTTGTCTGACGGTCTGATGACCATTAATCAACAGCAGCGGCTCGACATCTCTGTTAT 360
 316 GTTGTCTGACGGTCTGATGACCATTAATCAACAGCAGCGGCTCGACATCTCTGTTAT 375

Qy 361 CTGTCTGCGGTTTACGCAACCGGATGACGACTGCTGGCGGTGCGACCTGATGGCA 419
 376 CTGTCTGCGGTTTACGCAACCGGATGACGACTGCTGGCGGTGCGACCTGATGGCA 435

Db 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTTGGTTTGAACGCAACGNTAATGG 479
 436 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTTGGTTTGAACGCAACGNTAATGG 495

Qy 480 CCGGAGCGGGAATTTGCTGTGACAGACTCCGGGACNATGATCCCGTGATGCT 539
 496 CCGGAGCGGGAATTTGCTGTGACAGACTCCGGGACNATGATCCCGTGATGCT 554

Db 540 CCGCGGGGAACTTAATATACCCGCTGTCANANGAAGTTGCCCTCTGGATCCCTT 599

Db 555 CMCACGAGACCTTANATAGCCGTCATCC---ANGACTNCCCCTCTGGTCACTTT 610

Qy 600 TAAACNCAANTGAATCTCNCNTNANGAAGAACTCTTATGAACAGCTTTAANACNA 659

Db 611 TAAACNCAANTGAATCTCNCNTNANGAAGAACTCTTATGAACAGCTTTAANACNA 669

Qy 660 TCGATGACNACNGTCTCCTCCGTCACATTTGCCAATGGCGCTGCTACACNCAATT 717

Db 670 TCGATGGAC-CCGTGTCAACGTTCCNCTTGGCCCAATGGCGCTGCTACNCTNCTT 726

RESULT 8

A70155

LOCUS A70155 727 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 16 from Patent W09811228.

ACCESSION A70155

VERSION A70155.1 GI:4774570

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS 1 (bases 1 to 727)

TITLE Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.

JOURNAL GENETIC CONTROL OF FRUIT RIPENING

Patent: WO 9811228-A 16 19-MAR-1998;

SETMOUR GRAHAM BARON (GB)

FEATURES

source Location/Qualifiers

1..727

/organism="unidentified"

/db_xref="taxon:32644"

/clone="U-089"

BASE COUNT 145 a 205 c 196 g 159 t 22 others

ORIGIN

Query Match 67.5%; Score 543.8; DB 6; Length 727;

Best Local Similarity 86.6%; Pred. No. 9,8e-132;

Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 2 GTTCTCTCTCGATCACAATCTTTTGTCTGGAAACGTGAGAGTGAAGAGCGCG 61

Db 8 GTTCTCTCTCGATCACAATCTTTTGTCTGGAAACGTGAGAGTGAAGAGCGCG 67

Qy 62 CAATGAGCGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121

Db 68 CAATGAGCGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127

Qy 122 TGGTTTGAACGAGGTGGGGTGGATTGGAAGCAGAGGCTCTGCTGAGGAATG 181

Db 128 TGGTTTGAACGAGGTGGGGTGGATTGGAAGCAGAGGCTCTGCTGAGGAATG 187

Qy 182 GCGGAGCATCGCGAGGAGCTTGAAGAGGCTCCGCGAACGCGACGCGCGATGCTT 241

Db 188 GCGGAGCATCGCGAGGAGCTTGAAGAGGCTCCGCGAACGCGACGCGCGATGCTT 247

Qy 242 CCTTGAAGAGAGGCTTAAACCGCGGAGAGAGAGCGGAGTGAAGAGAGAGAG 301

Db 248 CCTTGAAGAGAGGCTTAAACCGCGGAGAGAGAGCGGAGTGAAGAGAGAGAG 307

Qy 302 TTGCTTCAGCGTCTCTGATGACATATCAACAGAGCGGCTCGCATCTCTTGGTTATC 361

Db 308 TTGCTTCAGCGTCTCTGATGACATATCAACAGAGCGGCTCGCATCTCTTGGTTATC 367

Qy 362 TGTGTGCGGTTTCAAGCAACCGATGACAGACTGCTGCGGTGCGACCTGATTTGGCATG 421

Db 368 TGTGTGCGGTTTCAAGCAACCGATGACAGACTGCTGCGGTGCGACCTGATTTGGCATG 427

Qy 422 TCAACAGAAAAAGTCTGCTGACATGCGGATTTGGCTTGG-AACGACGNNATANGTC 480

Db 428 TCAACAGAAAAAGTCTGCTGACATGCGGATTTGGCTTGGCCGCAACGCAATANGTC 487

Qy 481 CGGAGCGGGAATTTGTTGTTGAGACACTCGGCGGAGCAATATCCCGGATCTCTC 540

Db 488 CGGAGCGGGAATTTGTTGTTGAGACACTCGGCGGAGCAATAT-CCCGGATCTCTC 546

Qy 541 GCCCGGAACACTTANATACCCGCTCNCNTNANGAAGTGGCCCTCTGGATCCCTTT 600

Db 547 CCCCGGAACACTTANATATCCCGCTCNCNTNANGAAGTGGCCCTCTGGATCCCTTT 603

Qy 601 AAACNCAANTGAATCTCNCNTNANGAAGAACTCTTATGAACAGCTTTAANACNA 660

Db 604 AAACNCAANTGAATCTCNCNTNANGAAGAACTCTTATGAACAGCTTTAANACNA 662

Qy 661 CGATGACNACNGTCTCCTCCGTCACATTTGCCAATGGCGCTGCTACACNCAATT 717

Db 663 NATGACNACNGTCTCCTCCGTCACATTTGCCAATGGCGCTGCTACACNCAATT 722

Qy 721 TCCCG 725

Db 723 TCNCC 727

RESULT 9

A70157

LOCUS A70157 724 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 18 from Patent W09811228.

ACCESSION A70157

VERSION A70157.1 GI:4774572

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS 1 (bases 1 to 724)

TITLE Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.

JOURNAL GENETIC CONTROL OF FRUIT RIPENING

Patent: WO 9811228-A 18 19-MAR-1998;

SETMOUR GRAHAM BARON (GB)

FEATURES

source Location/Qualifiers

1..724

/organism="unidentified"

/db_xref="taxon:32644"

/clone="U-0117"

BASE COUNT 143 a 201 c 197 g 155 t 28 others

ORIGIN

Query Match 56.5%; Score 536; DB 6; Length 724;

Best Local Similarity 89.7%; Pred. No. 1,1e-129;

Matches 617; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

Qy 6 TCTCCTTGAACATCTTTTGTCTGGAAGAGTGAAGAGTGAAGAGGCGGCAAT 65

Db 9 TCTCCTTGAACATCTTTTGTCTGGAAGAGTGAAGAGTGAAGAGGCGGCAAT 68

Qy 66 GACGCGGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125

Db 69 GACGCGGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 128

Qy 126 TTTGAACGAGGTGGGGTGGATTGGAAGCAGAGGCTCTGCTGAGGAATGCGG 185

Db 129 TTTGAACGAGGTGGGGTGGATTGGAAGCAGAGGCTCTGCTGAGGAATGCGG 188

Qy 186 AGCATCGCGGAGAGCTTGAAGAGGCTCCGCGAACGCGACGCGCGATGCTCTT 245

Db 189 AGCATCGCGGAGAGCTTGAAGAGGCTCCGCGAACGCGACGCGCGATGCTCTT 248

Qy 246 GGAAGAGAGGCTGTAAACCGCGGAGAGAGCGGAGTGAAGAGAGAGAGTTC 305

Db 249 GGAAGAGAGGCTGTAAACCGCGGAGAGAGCGGAGTGAAGAGAGAGAGTTC 308

Qy 306 TTTGACGCTCTGATGACATATCAACAGAGCGGCTCGCATCTTGTATATCTGC 365

Db 309 TTTGACGCTCTGATGACATATCAACAGAGCGGCTCGCATCTTGTATATCTGC 368

Qy 366 GTGGGTTCAAGCAACCGGATGACAGACTGCTGCGGTGCGACCTGATTTGGATGCA 425

Db 369 GTGGGTTCAAGCAACCGGATGACAGACTGCTGCGGTGCGACCTGATTTGGATGCA 428

426 CAGAAAAAGCTGCTGACGCGGCAATGGCTTTGGACGCAACGCNATANGTGGCCGCGA 485
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429 CAGAAAAAGCTGCTGACGCGGCAATGGCTTTGGACGCAACGCNATANGTGGCCGCGA 488
|||||
486 CGGGGAATTTGTTGGTTGTGACAGACTCCGGGAGCAATGATCCCGGTGAATCTTCGCCG 545
|||||
489 CGGGG-AATTTGTTGGTTGTGACAGACTCCGGGAGCAATGATCCCGGTGAATCTTCGCCG 547
|||||
546 GGAACACTTANATATACCCGCTNTCCAAAGAGTTGGCCCTCTGGGATCCCTTTAAACN 605
|||||
548 GGAACACTTANAT-NCCCGCTNTCCNNAANTTTCCCTCT- -GATCNCCTTTAAAC 603
|||||
606 CNAANTGAAATCTCNCCTCNAANGAAGAACTCMTATGACAGC- -TTTAAACNATGA 663
|||||
604 C- -ACNTGANAATCCCCCNAGAAAGAACTCTATGACNGCTTTTAAACATGAT 661
|||||
664 TGACNCGTGTCTCTGTCACATGGC 691
|||||
662 NGACCCNGTTCACCTTCACATTTGC 689
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RESULT 10

LOCUS A83000 704 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9853085.
ACCESSION A83000
VERSION A83000.1 GI:6732480
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 704)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 7 26-NOV-1998;

FEATURES
SOURCE Location/Qualifiers
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/organism="unclassified"
/db_xref="taxon:32644"
/clone="U-12"

BASE COUNT 146 a 190 c 191 g 149 t 28 others
ORIGIN

Query Match 63.4%; Score 510.8; DB 6; Length 704;
Best Local Similarity 86.8%; Pred. No. 4.4e-123;
Matches 603; Conservative 0; Mismatches 86; Indels 6; Gaps 5;

10 CTTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGTGAGACGAGCGGCAATGACG 69
|||||
5 CTTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGTGAGACGAGCGGCAATGACG 64
|||||
70 GCGGGTTAAGATGATTCCTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 129
|||||
65 GCGGGTTAAGATGATTCCTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
|||||
130 AACGAGAGTGGGGGTGATTTGAAAGAGAGAGTCTCTGCTCGAGGAATGGCGAGCA 189
|||||
125 AACGAGAGTGGGGGTGATTTGAAAGAGAGAGTCTCTGCTCGAGGAATGGCGAGCA 184
|||||
190 TCGCGAGAGAGCTTTGAGAGAGGCTCCGCGAAGCGAGCAAGCGGATGCTTCTTGGAA 249
|||||
185 TCNCGAGAGAGCTTTGAGAGAGGCTCCGCGAAGCGAGCAAGCGGATGCTTCTTGGAA 244
|||||
250 GAGAGGCTGTATACCCGGGAGAGAGCGGAGTCCAGTCCAGGACCCCGAGAGAGTTGCTTCG 309
|||||
245 GACAGGGGTGTNACCGAGGAGAGAGCGGAGTCTNATGACCCCGAGAGAGTTGCTTCN 304
|||||
310 ACGGTCTGATGACCATTAATCAACAGACGAGCTCGAGATCTTTGGTTATCTGTCTGC 369
|||||
305 ACGGTCTGATGACCATTAATCAACAGACGAGCTCGAGAAATCTTTGGTTATCTGTCTGC 364
|||||
370 GGTTCAGGCAACCCGATCGACGACTGCTGGCGGTGCGACCTGATTTGGCATGTCAACAG- 428
|||||

|||||
365 GGTTCAGGCAACCCGATCGACNACTGCTGGGGTGGCGACCCGATTTGCGATGCAACAGA 424
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429 AAAAAAGCTGCTGACTCGGCGCATTTGGTTGGAGCGACAGCAACNATANGTGGCCGCGAGG 488
|||||
425 AAAAAAGCTGCTGACTCGGCGCATTTGGTTGGAGCGACAGCAACNATANGTGGCCGCGAGG 484
|||||
489 GGAATTTGTGCTGTGACAGACTCCGGGAGCAATGATCCCGGTGAATCTTCGCCGCGGGA 548
|||||
485 GG-AATTTGTGCTGTGACAGACTCCGGGAGCGATGAT-CCCGGTGAATCTTCGCCGCGGGA 542
|||||
549 ACACTTANATAC-CCCGTNTCCAAANGAAGTTGCCCTCTGGGATCCCTTTAAACN 607
|||||
543 ACACTTANATACNCCCGTCANCCANGAAGT- -GCCCTCTGGGATCCTTTAAACCC 600
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608 AANTGGAATCTCNCCTCNAANGAAGAACTCTTATGAACACTTTAANAATGATGGA 667
|||||
601 ACNTGANAATCTCCGCTCNAANGAAGAACTCTTATGACNCTTTTAAACATGCA 660
|||||
668 CNCNGTCTCTGTCACATTTGCCATGGCGCTG 702
|||||
661 ATGACNCCNGTTCACCTTCACATTTGCCANTG 695
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RESULT 11

LOCUS A83012 706 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 19 from Patent WO9853085.
ACCESSION A83012
VERSION A83012.1 GI:6732492
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 706)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 19 26-NOV-1998;

FEATURES
SOURCE Location/Qualifiers
1..706
/organism="unclassified"
/db_xref="taxon:32644"
/clone="U-114"

BASE COUNT 144 a 192 c 195 g 153 t 22 others
ORIGIN

Query Match 61.6%; Score 496.8; DB 6; Length 706;
Best Local Similarity 90.6%; Pred. No. 2.1e-119;
Matches 639; Conservative 0; Mismatches 52; Indels 14; Gaps 10;

2 GTTCTCTCTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGTGAGACGAGGCGG 61
|||||
7 GTTCTCTCTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGTGAGAGGCGGCGG 66
|||||
62 CAATGACGCGGGTTTAAGATGATTCCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 121
|||||
67 CAATGACGCGGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
|||||
122 TGGTTTGAACGGAAGTGGGGGTGATTTGAAAGCGAGAGGCTCTTGGCTCGAGGAATG 181
|||||
127 TGGTTTGAACGGAAGTGGGGGTGATTTGAAAGCGAGAGGCTCTTGGCTCGAGGAATG 186
|||||
182 GCGGAGCATTCGCGGAGAGGCTTTGAGAGAGGCTCCGCGAAGCGGACCGGCGCATGCTT 241
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187 GCGGAGCATTCGCGGAGAGGCTTTGAGAGAGGCTCCGCGAAGCGGACCGGCGCATGCTT 246
|||||
242 CTTTGAAGAGAGGCTTAAACCCGGGAGAGAGCGGAGTCTGACGAGACCCCGAGAGG 301
|||||
247 CTTTGAAGAGAGGCTTAAACAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGG 306
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302 TTGCTTACAGGCTCTGATGACATTAATCAACAGACGAGCTCGAGATCTTGGTTATC 361
|||||

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Db 307 TTGCTTCGACGGCTCTGACGACCATATATACAGCAGCGGCTCCGACATCTCTTGTTATC 366
QY 362 TGTGTCGCGGTTCCAGGCAA-CCCGATCGAGAGCTGCTGGCGGTG-CGACCTGATTGGCA 419
Db 367 TGTGTCGCGGTTCCAGGCAA-CCCGATCGAGAGCTGCTGGCGGTG-CGACCTGATTGGCA 426
QY 420 TGTCAACACAAAAAAGCTGCTGACGCGGCAATTGGC-TTGGAGCCAGACGAAATGNGTG 478
Db 427 TGTCAACACAAAAAAGCTGCTGACGCGGCAATTGGC-TTGGAGCCAGACGAAATGNGTG 486
QY 479 GCGGCG--GAGCGGGAATTTGTTGCTG-TGACAGACTCC-GGGAGACNATGATCCCGTGA 534
Db 487 GCGGCGGAGCGGGAATTTGTTGCTG-TGACAGACTCC-GGGAGAGATGATCCCGTGA 546
QY 535 ATCTGCGCC--GGGACACTAATATACCCCGCTGCTCAANGAAGTTGCCCTGCGGA 592
Db 547 ATCTGCGCC--GGGACACTAATATACCCCGCTGCTCAANGAAGTTGCCCTGCT--GGA 603
QY 593 TCCCTTTAAGCNAATGAAATCTGCTGCTCAANGAAGTTGCCCTGCTGATGACACTTT 652
Db 604 TCCCTTTAAGCNAATGAAATCTGCTGCTCAANGAAGTTGCCCTGCTGATGACACTTT 661
QY 653 AANACNATGAGAGACNCGTGTCTGCTCAANGAAGTTGCCCTGCTGATGACACTTT 697
Db 662 AANACATCAATGAGNCGTGTCTGCTCAANGAAGTTGCCCTGCTGATGACACTTT 706

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RESULT 12
LOCUS OSJN00272/c 127202 bp DNA linear HTG 17-JUN-2002
DEFINITION Oryza sativa chromosome 4 clone OSJNB0095E20, *** SEQUENCING IN
PROGRESS ****, 4 ordered pieces.
ACCESSION AL731627
VERSION AL731627.2 GI:21743085
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE

AUTHORS

Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Meng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, X., Hu, H., Jia, P.X., Qian, Y.M., Ying, R., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, D.P., Fu, G., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H. and Hong, G.F.

TITLE

JOURNAL

Direct Submission
Submitted (27-JUN-2002) Han Bin, National Center for Gene Research,
Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSJNB0095E20.
On Jul 12, 2002 this sequence version replaced gi:20452125.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics

REMARK

COMMENT

Assembly program: phrap

NOTE: This is a PHASE2 sequence. Gaps are shown by nnnn. Genes
were identified by a combination of several methods: Gene
prediction programs including Egenes (http://www.softberry.com/),
genscan (http://CCR-081.mit.edu/GENSCAN.html), GENSCANM (http://genemark.biology.gatech.edu/genemark/), GENSCAN-SE (Sean
Eddy, http://genome.wustl.edu/eddy/GENSCAN-SE/), searches of the
complete sequence against NCBI non-redundant protein database (nr)
(ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs

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* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 82614: contig of 82614 bp in length
82615 82614: gap of 200 bp
82815 84736: contig of 1922 bp in length
84737 84936: gap of 200 bp
84937 93650: contig of 8714 bp in length
93651 93650: gap of 200 bp
93851 127202: contig of 33352 bp in length.
Location/Qualifiers
1. 127202
/organism="Oryza sativa"
/variety="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="4"
/clone="OSJNB0095E20"
/clone_1kb="CDG-OSJNB"
BASE COUNT 37100 a 25541 c 26047 g 37909 t 605 others
ORIGIN

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Query Match 21.6%; Score 174.4; DB 2; Length 127202;
Best local similarity 68.0%; Pred. No. 7.6e-35;
Matches 299; Conservative 0; Mismatches 133; Indels 8; Gaps 5;

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Db 51989 GGCTGCGCGACGCTGCGGACGCTGCTGCGGACGCTGCTGCGGACGCTGCT 51931
QY 494 TTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
Db 51930 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 51872
QY 554 TAAATACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
Db 51871 CCGGTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 51816
QY 614 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
Db 51815 TGATCAGCTC-AAGCAGAGCTGATGATGATGATGATGATGATGATGATGATG 51757
QY 674 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
Db 51756 GCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 51698
QY 734 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
Db 51697 CATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 51678

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RESULT 13

LOCUS

AY085026

DEFINITION

Arabidopsis thaliana clone 124816 mRNA, complete sequence.

ACCESSION

AY085026.1

VERSION

AY085026.1

KEYWORDS

FLI CDNA.

SOURCE

thale cress.

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1633)
 Haas, B.J., Volkovskiy, N., Town, C.D., Troughan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome annotation
 Genome Biol. (2002) In press
 2 (bases 1 to 1633)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 Full-length cDNA from Arabidopsis thaliana
 Unpublished
 3 (bases 1 to 1633)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 Direct Submission
 Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
 This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
 Location/Qualifiers
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 STGSSHTWIDHNSLNCADGLDVAVSTAIYVSNFEFTHNNSVMLGSDSTTRK
 VMQVTLAVNHGGLIQMRPCRHRGYFHVYNNDYTHMEMTAIGSAPPTINSQNRFL
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 KSSSLVGTMTSYSGALNCRAGRRIC"
 BASE COUNT 434 a 375 c 344 g 480 t
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 Best Local Similarity 63.5%; Pred. No. 1.5e-33;
 Matches 304; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

423 GGAATTTTCCCGCAACGCAATCGAGCGCGAC-GTTCGTTTCTACCTCGTAACGACCC 481
 514 CGGGAGNANGATATCCCGTGAACTCCGCCCGGGAACAATTAATACCCGTCMTCCAN 573
 482 TGGAGACGACAT-CCGTTATCTCCATACCGGGAACATCGCTACGCGCTGATTC- 537
 574 GAAGTTCCTCCCTCTGGATCCCTTTAAACNCAANTGAAATCTCNCNANGAAGA 633
 538 -AAGACGACACATCTGGATCATCTTCAACGACACATGGTTATAC-CTTGAAAGACA 595
 634 ACTCATTATGACAGCTTTTAANACNATGATGACNCGTCTCTGTCATGGCAA 693
 596 GCTATCATGAAAGCTTCAAAACCATGATGATGCTGCTGATGATGATGATGAT 655
 694 TGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 656 TGGAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
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 DEFINITION Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence,
 complete sequence.
 ACCESSION AC016827
 VERSION AC016827.7 GI:12408743
 KEYWORDS HMG.
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases: 1 to 90142)
 Lin, X., Kaul, S., Town, C.D., Beilto, M.-I., Creasy, T.H., Haas, B.,
 Wu, D., Rensing, C.M., Koo, H., Fujii, C.Y., Ulteback, T.R.,
 Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
 Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence
 Unpublished
 2 (bases: 1 to 90142)
 Lin, X. and Kaul, S.
 Direct Submission
 Submitted (08-DEC-1999) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA, xlin@tigr.org
 3 (bases: 1 to 90142)
 Lin, X.
 Direct Submission
 Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Jan 24, 2001 this sequence version replaced g1:12280775.
 Address all correspondence to: atet@tigr.org
 BAC clone: F17A9 is from Arabidopsis chromosome III and is near the
 molecular marker m1357.
 The orientation of the sequence is from Sp6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of three methods: Gene
 prediction programs including GRLIT (available by anonymous ftp
 from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of
 Washington), Genscan (Chris Burge,
 http://genome.stanford.edu/~chris/GENSCANW.html), and NetPlantGene
 (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the
 complete sequence against a peptide database and the Arabidopsis
 EST database at TIGR (http://www.tigr.org/tdb/at/est.html).
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as 'unknown' proteins.
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as 'hypothetical' proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are


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Query Match
  18.9%: Score 152; DB 8; Length 90142;
Best Local Similarity 63.5%; Pred. No. 5.6e-29;
Matches 277; Conservative 0; Mismatches 152; Indels 7; Gaps 4;

QY 317 TGATGACCAATATACAGACAGCGCTCGCAGATCTCTGTTATCTCTGCGGTTGAG 376
DB 53474 TCAGGACATTTGAAACAGACAGAGAGAGAAATAGTTACTTCTCTGCGGCAACG 53415
QY 377 GCAACCGGATCGACGACTGCTGGCGGTGCGACCTGATGGCAGTCAACAGAAAAAGC 436
DB 53414 GCAACCGGATCGACGACTGCTGGCGGTGCGACCTGATGGCAGTCAACAGAAAAAGC 53355
QY 437 TCGGTGACTGGGCGATGGGCTTTGGACGCAACGCAATANGTGGCGGAGGGAATTTG 496
DB 53354 TAGCCGATTTGCTCAATGAGATTTGGCCGCAACGCAATGAGGCGCGAC-GGTCGTTTC 53296
QY 497 TTGCTGTGACAGACTCGGGGACNATGATCCCGTGAATCTCGCCGGGACACTTAN 556
DB 53295 TAGCTGTAACCGACCTGGAGACGAGAT-CCGTTAATCCCATACGGGACACTCCG 53237
QY 557 ATACCCGCTCCTCCANAGAGTTGCCCTCTGGGATCCCTTTAAACNCAANTGAAA 616
DB 53236 TCACGCGGTGATTC---AAGACGACACCTCTGATCATCTCAACGCGACATGGTTA 53181
QY 617 TCTGCTCNANGAAGAACTNTATGACAGCTTTAANCAACNATGAGACNCGTGC 676
DB 53180 TAAC-CTTGAACGACGAGCTGATCATGACAGCTTCAAAACCAATGAGTGGTGGTGC 53122
QY 677 CTGCTGCAATTCGCAATGGCGCTGCTGNTCACACCAATTTCTCCCAACNTCTT 736
DB 53121 AATGTTCAATCGCTAATGAGGTTGTTCTCACGATTCATACGTTACGACATATATGTC 53062
QY 737 CCATNGCCTCCNCCTCC 752
DB 53061 CATTGGATTCATGTC 53046

RESULT 15
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LOCUS A83003 823 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 10 from Patent WO9853085.
ACCESSION A83003
VERSION A83003.1 GI:6732483
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 823)
AUTHORS Seymour G.B. and Bird C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 10-26-NOV-1998;
SETMOOR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
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Best Local Similarity 63.7%; Pred. No. 9.9e-29;
Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

QY 327 AATCAACAGACGGCTCGCAGATCTTGGTTATCTGCTGCGTTCAAGCAACCGAT 386
DB 137 AAGCTTAACGCTGCGCGGCGGAGCTGGGCTACTGTCAACCGGCAATCCGAT 196
QY 387 CGACGACTGCTGGCGGCTGCCACCTGATTTGGCATGTCAACGAAAAAGCTCGCTGACTG 446
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DB 197 CGACGACTGCTGGGCGGTGGCCGATCCTGACTGGGCGGCAACCGGAGCGGCTCGGACTG 256
QY 447 CGGCTATGGCTTTGACGCAACGCAATANGTGGCGGAGCGGGAATTTGTTGTTGGA 506
DB 257 CGCATCGGCTTGGGGAAGACGCGATTTGGGGGAGGAGCGCG-AGATATACGTGGTGA 315
QY 507 CAGACTCGGGGACNATGATCCCGTGAATCCTGCGCGGAGCACTTANATACCGCTC 566
DB 316 CCGACAGTGGCGAGACGA-CCCGTCAATCCGAAGCGGSCACGCTCCGTTACGCCGTC 374
QY 567 TTCANAGAGTTGCCCTCTGGGATCCCTTTAAACNCAANTGAAATCTGCTGNA 626
DB 375 ATCCAGGAGGAGCGCGCTGT---GATCATCTTCAAGCGGACATGTCATC-CAGTTGA 430
QY 627 NGAGAAGACTNTATGACAGCTTTAANCAACNATGAGACNCGTCTCTGCTGACA 686
DB 431 AGGAGAGCTTATATGAACTCCCAAGACATGAGAGGCGGCGGCGGCTCCACA 490
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DB 491 TCTCCGGGCGGCGGTGATGACATCCACATCCAGTAGTCAACCAATCATCATCAGGGGTC 550
QY 747 CACTGCC 753
DB 551 CACATCC 557
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Search completed: June 24, 2003, 01:52:02
Job time : 2215 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 22:19:35 ; Search time 252 Seconds
(without alignments)
7202.820 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
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Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	96.5	806	19 AAV28655	Ripening banana pu
2	591.8	73.4	748	20 AAV69457	Banana fruit ripen
3	591.2	73.3	745	20 AAV69450	Banana fruit ripen
4	588.8	73.1	793	20 AAV69447	Banana fruit ripen
5	572.2	71.0	727	20 AAV69460	Banana fruit ripen
6	543.8	67.5	727	19 AAV28658	Ripening banana pu
7	536	66.5	724	19 AAV28660	Ripening banana pu
8	510.8	63.4	704	19 AAV28660	Banana fruit ripen
9	496.8	61.6	706	20 AAV69458	Banana fruit ripen

10	169.4	21.0	1633	21 AAC36622	Arabidopsis thalia
11	151	18.7	823	20 AAV69449	Banana fruit ripen
12	148.8	18.5	1526	21 AAC42069	Arabidopsis thalia
13	144.4	17.9	749	20 AAV69445	Banana fruit ripen
14	142.8	17.7	842	19 AAV28659	Ripening banana pu
15	141.4	17.5	708	20 AAV69448	Banana fruit ripen
16	141	17.5	1521	21 AAC49440	Arabidopsis thalia
17	134.6	16.7	687	19 AAV28656	Ripening banana pu
18	131.6	16.3	772	20 AAV69456	Banana fruit ripen
19	131	16.3	758	20 AAV69451	Banana fruit ripen
20	130.4	16.2	1233	21 AAC46041	Arabidopsis thalia
21	130.4	16.2	1323	21 AAC51583	Arabidopsis thalia
22	129.2	16.0	794	20 AAV69452	Banana fruit ripen
23	128.8	15.9	728	20 AAV69459	Banana fruit ripen
24	128.4	15.9	745	20 AAV69454	Banana fruit ripen
25	127	15.8	1779	21 AAC45923	Arabidopsis thalia
26	126.2	15.7	731	20 AAV69455	Banana fruit ripen
27	124.6	15.5	1786	21 AAC40484	Arabidopsis thalia
28	124	15.4	1440	20 AAC07385	Zinnia elegans pec
29	120.8	15.0	1359	21 AAC50766	Arabidopsis thalia
30	119.4	14.8	710	20 AAV69453	Banana fruit ripen
31	118.4	14.7	1413	21 AAC51079	Arabidopsis thalia
32	116.4	14.4	1257	21 AAC42899	Arabidopsis thalia
33	116.4	14.4	1317	21 AAC30849	Arabidopsis thalia
34	114.6	14.2	1514	21 AAC41563	Arabidopsis thalia
35	113	14.0	1615	21 AAC51025	Arabidopsis thalia
36	113	14.0	1617	21 AAC41994	Arabidopsis thalia
37	110.4	13.7	1221	21 AAC47293	Arabidopsis thalia
38	110.4	13.7	1631	21 AAC33659	Arabidopsis thalia
39	110.4	13.7	1631	21 AAC49928	Arabidopsis thalia
40	109.6	13.6	1125	21 AAC42903	Arabidopsis thalia
41	94	11.7	438	21 AAA31518	Plant microsatellit
42	93.4	11.6	460	24 ABL93674	Arabidopsis thalia
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45	81.8	10.1	1523	21 AAC31573	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAV28655 standard; CDNA; 806 BP.
AC AAV28655;
XX
XX 29-JUL-1998 (first entry)
XX
XX Ripening banana pulp cDNA clone U-068 SEQ ID NO:13.
XX
XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
XX genetic control; tissue senescence; ss.
XX
XX Musa acuminata.
XX
XX WO9811228-A2.
XX
XX PD 19-MAR-1998.
XX
XX PF 08-SEP-1997; 97WO-GB02424.
XX
XX 25-APR-1997; 97GB-0008366.
XX PR 10-SEP-1996; 96GB-0018862.
XX
XX (ZENE) ZENECA LTD.
XX
XX PA Bird CR, Medina-Suarez RDJ, Seymour GB;
XX WPL; 1998-207389/18.
XX
XX PT Modulation of ripening or tissue senescence in bananas - comprises
use of DNA isolated from ripening banana pulp to produce genetically

modified fruit

Claim 1: Page 26; 72pp; English.

The present sequence represents a cDNA clone isolated from ripening banana pulp. 57 clones were isolated and are given in AAV28643 to AAV28659. The cDNA clone sequences can be used in a method of modulating ripening or tissue senescence processes in plants of the genus *Musa*. The method comprises: (a) inserting into the plant material at least 1 of the 57 sequences (as above); (b) regenerating the plant material, and (c) selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics. Also described in the present invention are: (1) plants, their progeny, seed and material obtained from the plants, produced by the above method; (2) a vector functional in plants comprising a promoter region which is operably in plant cells, a polynucleotide sequence as defined above, and a transcription termination sequence; and (3) a method of controlling plant pathogens comprising the application of anti-pathogenic agent to plants of (1).

Sequence 806 BP; 157 A; 229 C; 212 G; 180 T; 28 other;

Query Match 96.5%; Score 778; DB 19; Length 806;
Best Local Similarity 100.0%; Pred. No. 1e-221;
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 60
1 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 60

61 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120
61 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120

121 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAACGAGAGTCTCTGCGTCTGAGGAT 180
121 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAACGAGAGTCTCTGCGTCTGAGGAT 180

181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGCGCTCCGGAACGAGAGCGCCGATCT 240
181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGCGCTCCGGAACGAGAGCGCCGATCT 240

181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGCGCTCCGGAACGAGAGCGCCGATCT 240
181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGCGCTCCGGAACGAGAGCGCCGATCT 240

241 TCCCTTGAAGAGAGGCTGTAAACCGGGCAGAGAAAGCGCGATGAGAGAGAGAGAG 300
241 TCCCTTGAAGAGAGGCTGTAAACCGGGCAGAGAAAGCGCGATGAGAGAGAGAGAG 300

241 TCCCTTGAAGAGAGGCTGTAAACCGGGCAGAGAAAGCGCGATGAGAGAGAGAGAG 300
241 TCCCTTGAAGAGAGGCTGTAAACCGGGCAGAGAAAGCGCGATGAGAGAGAGAGAG 300

301 GTTGTCTGACGAGTCTGATGACATTAATCAACAGACAGCGCTCGAGATCTTGTAT 360
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301 GTTGTCTGACGAGTCTGATGACATTAATCAACAGACAGCGCTCGAGATCTTGTAT 360
301 GTTGTCTGACGAGTCTGATGACATTAATCAACAGACAGCGCTCGAGATCTTGTAT 360

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361 CTGTCTGCGGTTGAGGAGACCGGATGAGAGAGTCTGCGGATGAGAGAGAGAGAG 420

361 CTGTCTGCGGTTGAGGAGACCGGATGAGAGAGTCTGCGGATGAGAGAGAGAGAG 420
361 CTGTCTGCGGTTGAGGAGACCGGATGAGAGAGTCTGCGGATGAGAGAGAGAGAG 420

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421 GTCAACAAAAAACTGCTGACTGCGGATGCTTGTGAGAGAGAGAGAGAGAGAGAG 480

421 GTCAACAAAAAACTGCTGACTGCGGATGCTTGTGAGAGAGAGAGAGAGAGAGAG 480
421 GTCAACAAAAAACTGCTGACTGCGGATGCTTGTGAGAGAGAGAGAGAGAGAGAG 480

481 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 540
481 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 540

481 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 540
481 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 540

541 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 600
541 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 600

541 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 600
541 GCGGAGGAGAAATTTGCTGTTGAGAGAGTCCGGGAGAGAGAGAGAGAGAGAGAG 600

601 AAACNCAANTGAAATCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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601 AAACNCAANTGAAATCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 AAACNCAANTGAAATCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

661 CGATGAG 720
661 CGATGAG 720

661 CGATGAG 720
661 CGATGAG 720

721 TCCCAACNTCTCTCTCCNTGCTCTCCNTGCTCTCCNTGCTCTCCNTGCTCTCCNTG 780
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721 TCCCAACNTCTCTCTCCNTGCTCTCCNTGCTCTCCNTGCTCTCCNTGCTCTCCNTG 780

781 CCCNCTCCCTG 806
781 CCCNCTCCCTG 806

781 CCCNCTCCCTG 806
781 CCCNCTCCCTG 806

RESULT 2
AAV69457
ID AAV69457 standard; cDNA; 748 BP.
AAV69457;
15-MAR-1999 (first entry)

Banana fruit ripening-related clone U-113 cDNA.
Fruit ripening; banana; modulator; tissue senescence; crop; plant;
triploid; plant breeding; ss.
Musa acuminata.
W09853085-A1.
26-NOV-1998.
05-MAY-1998; 98WO-GB01297.
20-MAY-1997; 97GB-0010370.
(ZENEC) ZENEC LTD.
Bird CR, Medina-Suarez RDJ, Seymour GB.
WPI: 1999-059745/05.
New method of modulating fruit ripening or tissue senescence characteristics of *Musa* plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening characteristics
Claim 1: Page 29; 78pp; English.
AAV69440-69512 are cDNA sequences which are used in a method to modulate the fruit ripening or tissue senescence characteristics of *Musa* acuminata (banana) plants. The method provides a recombinant way of modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such characteristics in the desert banana, which due to its triploid nature is unaffected by conventional plant breeding techniques.

Sequence 748 BP; 154 A; 211 C; 206 G; 163 T; 14 other;

Query Match 73.4%; Score 591.8; DB 20; Length 748;
Best Local Similarity 91.7%; Pred. No. 3.4e-166;
Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

1 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 60
1 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 60

16 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 75
16 TGTCTCTCTCTGATCATCATCTTTTGTCTGTGGAACGTGAGAGTGAGAGAGGCG 75

61 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120
61 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120

76 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 135
76 GCAATGAGAGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 135

121 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAAGCGAGAGTCTCTGAGAGAGAT 180
121 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAAGCGAGAGTCTCTGAGAGAGAT 180

136 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAAGCGAGAGTCTCTGAGAGAGAT 195
136 CTGTTTGAACGAGAGTGCGGGGTGATTTGGAAGCGAGAGTCTCTGAGAGAGAT 195

181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGAGCTCCGGAACGAGAGAGAGAGAT 240
181 GCGGAGAGATCGCGGAGAGAGCTTGTGAGAGAGAGCTCCGGAACGAGAGAGAGAT 240

Db		196	GCCGGAGCATCGCGGAGGAGCTTGAGAGAGGGCCTCCGCCAAGCGCAACGCGGCATTCGT	255
Oy		241	TCCTTGGAAAGAGAGGGCTGTAAACCCGGGGAGAGAAAGCCGCACTGCACGACCCCGAGAG	300
Db		236	TCCTTGGAAAGAGAGGGCTGTAAACAGGGGAGAGAAAGCCGCACTGCACGACCCCGAGAG	315
Oy		301	GTTCGTTTGACGCGTCTGTATGACCACTTAATCAACAGACGCGTCCGAGATCTCTTGGTTAT	360
Db		316	GTTCGTTTGACGCGTCTGTATGACCACTTAATCAACAGACGCGTCCGAGATCTCTTGGTTAT	375
Oy		361	CTGTCTGCGGTTTCAGGCAACCCGATCGACACTGCTGGCGGTGCGACCCTGATTGGCAT	420
Db		376	CTGTCTGCGGTTTCAGGCAACCCGATCGACACTGCTGGCGGTGCGACCCTGATTGGCAT	435
Oy		421	GTCAAACAGAAAAAACCTCGCTGACAGCGGCACTTGGCTTTGGAGCGCAACGCMNTANGTGGC	480
Db		436	GTCAAACAGAAAAAACCTCGCTGACAGCGGCACTTGGCTTTGGAGCGCAACGCGATAGGTGGC	495
Oy		481	CGCGACGGGGGAATTTTGTTCGTTGTGACAGACTCCGGGGAGCMNATGATCCCCGTGAATCTTC	540
Db		496	CGCGACGGGGGAATTTTGTTCGTTGTGACAGACTCCGGGGAGCMNATGATCCCCGTGAATCTTC	555
Oy		541	GCCGGGGGAACCTTANATAACCCGCTGTCNTCCAANGAATTGGCCCCCCTCTGTGGGATCCCCTT	600
Db		556	CCCCGGGGAACCTTANATAACCCGCTGTCATCCAGACTG-----CCCTCTGGAATCNCCTTT	610
Oy		601	AACNCNANTNGAATATCTCNCNTCNANGGAAGACGCMNTTATGAACAGCTTTAANCNAT	660
Db		611	AAACGCCACNTGAGNATCACCTCCA-GGAAGAAGCTCNTTATGAACAGCTTTAANAACAT	669
Oy		661	CGATGACNCNGTGTCTGTCTGCACATTGCCAATGGCGCCTGCNTCACCACCAATTTGN	720
Db		670	CGATGAGAC-CCGTGTTCAAGTCCACTTGGCCAAATGGC-CCTGCMTCACCATCCANNMNT	727
Oy		721	TCOC 724	
Db		728	CACC 731	
<hr/>				
RESULT 3				
AAV69450				
ID		AAV69450	standard; cDNA; 745 BP.	
XX		AAV69450;		
AC		15-MAR-1999	(first entry)	
XX				
DT		Banana fruit ripening-related clone U-52 cDNA.		
DE				
XX		Fruit ripening; banana; modulator; tissue senescence; crop; plant;		
KW		triploid; plant breeding; ss.		
XX		Musa acuminata.		
OS				
XX		WO9853085-A1.		
PN		26-NOV-1998.		
XX				
PD		05-MAY-1998;	98WO-GB01297.	
XX				
PE		20-MAY-1997;	97GB-0010370.	
PR				
XX		(ZENEC) ZENECA LTD.		
PA				
XX		Bird CR, Medina-Suarez RDU, Seymour GB;		
PI				
XX		WPI; 1999-059745/05.		
DR				
XX		New method of modulating fruit ripening or tissue senescence		
PT		characteristics of Musa plants - by introducing DNA sequences,		
PT		useful in processes for modifying plant/fruit ripening		
XX		characteristics		

XX Claim 1; Page 24-25; 78pp; English.

ps

cc AAV69440-v69512 are cDNA sequences which are used in a method to

cc modulate the fruit ripening or tissue senescence characteristics of Musa

cc acuminata (banana) plants. The method provides a recombinant way of

cc modulating ripening/senescence characteristics of bananas, which are a

cc globally important crop. In particular, the method can modulate such

cc characteristics in the dessert banana, which due to its triploid nature

cc is unaffected by conventional plant breeding techniques.

xx

xx Sequence 745 BP; 153 A; 204 C; 203 G; 163 T; 22 other;

xx

Query Match 73.3%; Score 591.2; DB 20; Length 745;

Best Local Similarity 90.5%; Pred No. 5.2e-166;

Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5

QY 1 TGTTCCTCCCTCGATCACAATCTTTTGGTCTGAGAAACGTGAGAGTGAGAGGCG 60

DB 7 TGTTCCTCCCTCGATCACAATCTTTTGGTCTGAGAAACGTGAGAGTGAGAGGCG 66

QY 61 GCAATGAGAGGGGGGTTTAAGATGATTCCTCTCTGCTTCTTCTTCTGGGCTTCTG 120

DB 67 GCAATGAGAGGGGGGTTTAAGATGATTCCTCTCTGCTTCTTCTTCTGGGCTTCTG 126

QY 121 CTGCTTTGAACGAGAGGTCGGGGGGGATTTGGAACGAGAGTCCCTGCGTCGAGAAAT 180

DB 127 CTGCTTTGAACGAGAGTCTGGGGGGTGATTTGGAACGAGAGTCTCTTGTCTGAGAAAT 186

QY 181 GCGGAGCATCGCGGAGGAGCTTTGAGAGAGGCTCCGCGAAGCGAGCCGCGATGCT 240

DB 187 GCGGAGCATCGCGGAGGAGCTTTGAGAGAGGCTCCGCGAAGCGAGCCGCGATGCT 246

QY 241 TCCCTGGAAGAGAGGGCTGTAAACCGGGGAGAGAAAGCCGAGTGAGAGACCCGAGAG 300

DB 247 TCCTTGGAAAGAGGGCTGTAAACCGGGGAGAGAAAGCCGAGTGAGAGACCCGAGAG 306

QY 301 GTTGTCTGAGCGTCTGATGACCAATTAACAACAGCAGCGCTCGAGATCTCTTGATT 360

DB 307 GTTGTCTGAGCGTCTGATGACCAATTAACAACAGCAGCGCTCGAGATCTCTTGATT 366

QY 361 CTGTGTGCGGTTTCAAGGGAACCCGATGCAAGCATCTGCGGTGGGACCTGATGGCAT 420

DB 367 CTGTGTGCGGTTTCAAGGGAACCCGATGCAAGCATCTGCGGTGGGACCTGATGGCAT 426

QY 421 GTCAACAG-AAAAAAGCTCGTGAATGGGCAATTGGCTTTGGACCAAGCATANGTGG 479

DB 427 GTCAACAGAAAAAAGCTCGTGAATGGGCAATTGGCTTTGGACCAAGCATANGTGG 486

QY 480 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGACNATATCCCGGTGAATCT 539

DB 487 CCGGAGCGGGG-ANTTGTACGTTGTGACAGACTCCGGGACNATAT-CCCGTGAATCT 544

QY 540 CGCGCGGGAACCTTAAATACCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 599

DB 545 CCGCGCGGAACCTTAAATACCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600

QY 600 TAAACNCAATGGAATCTCNCCTNANGAAGAACTGTTATGAACAGC---TTTANA 656

DB 601 TAAACNCAATGGAATCTCNCCTNANGAAGAACTGTTATGAACAGC---TTTANA 660

QY 657 CNAATGATGAGACNCGTCTCTGCTGTCACATTTGCCAATTTGGCCCTGCAACCAAT 716

DB 661 ACATGTGAGAGCCCGTGTTCNCNCTCAACATTTGCCAATTTGGCCCTGCTTACCATTCNAT 720

QY 717 TTCNTCCCAACNTCTCTCCNT 740

DB 721 TACATCACCAAGTATCTCTCAT 744

RESULT 4

AAV69447

ID AAV69447 standard; cDNA; 793 BP.

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XX AA69447;
AC 15-MAR-1999 (first entry)
DT Banana fruit ripening-related clone U-22 cDNA.
DE Fruit ripening; banana; modulator; tissue senescence; crop; plant;
KM triploid; plant breeding; ss.
XX Musa acuminata.
OS WO9853085-A1.
PN 26-NOV-1998.
PD 05-MAY-1998; 98WO-GB01297.
PF 20-MAY-1997; 97GB-0010370.
XX (ZENB ) ZENECA LTD.
PI Bird CR, Medina-Suarez RDJ, Seymour GB;
XX WPI; 1999-059745/05.
DR New method of modulating fruit ripening or tissue senescence
XX characteristics of Musa plants - by introducing DNA sequences,
PT useful in processes for modifying plant/fruit ripening
PT characteristics
XX
PS Claim 1; Page 22-23; 78pp; English.
XX AA69440-V69512 are cDNA sequences which are used in a method to
CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC acuminata (banana) plants. The method provides a recombinant way of
CC modulating ripening/senescence characteristics of bananas, which are a
CC globally important crop. In particular, the method can modulate such
CC characteristics in the desert banana, which due to its triploid nature
CC is unaffected by conventional plant breeding techniques.
XX
SQ Sequence 793 BP; 170 A; 222 C; 215 G; 171 T; 15 other;
Query Match 73.1%; Score 588.8; DB 20; Length 793;
Best Local Similarity 88.7%; Pred. No. 2.8e-165;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
OY 1 TGTCTCTCCTCGATGACATCTTTTGTCTGGGAAAGTGAGAGGAGGAGGCG 60
DB 8 TGTCTCTCCTCGATGACATCTTTTGTCTGGGAAAGTGAGAGGAGGAGGCG 67
OY 61 GCATGACGCGGGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTG 120
DB 68 GCATGACGCGGGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTG 127
OY 121 CTGCTTTTGAAGAGGAGGTCGGGGTGATGGAACGAGAGGTCCTTGGCTCGAAGAT 180
DB 128 CTGCTTTTGAAGAGGAGGTCGGGGTGATGGAACGAGAGGTCCTTGGCTCGAAGAT 187
OY 181 GCGCGAGCATCGCGAGAGAGCTTGAAGAGGCTCCGGAACGAGCAGCGCCGATGCT 240
DB 188 GCGCGAGCATCGCGAGAGAGCTTGAAGAGGCTCCGGAACGAGCAGCGCCGATGCT 247
OY 241 TCTTTGAAGAGAGGGCTGTAAACCGGAGCAGAGAGCGAGTGCAGCAGCCGAGGAG 300
DB 248 TCTTTGAAGAGAGGGCTGTAAACCGGAGCAGAGAGCGAGTGCAGCAGCCGAGGAG 307
OY 301 GTTGTGTCGAGCGTCTCATATGACATTAATCAACAGCAGCGCTCCGAGATCTTTGTTAT 360
DB 308 GTTGTGTCGAGCGTCTCATATGACATTAATCAACAGCAGCGCTCCGAGATCTTTGTTAT 367
OY 361 CTGTGTCGAGCGTCTCATATGACATTAATCAACAGCAGCGCTCCGAGATCTTTGTTAT 420

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DB 368 CTGTGTCGAGCGTCTCATATGACATTAATCAACAGCAGCGCTCCGAGATCTTTGTTAT 427
OY 421 GTCAACAG-AAAAAGCTGCTGACTGCGGCGATTGGCTTTGGAGCCAAAGCNAATANGTG 479
DB 428 GTCAACAGAAAAAGCTGCTGACTGCGGCGATTGGCTTTGGAGCCAAAGCNAATANGTG 487
OY 480 CCGCGAGCGGGAATTTGTTGTTGTCAGAGACTCCGGGAGCANTAGTCCGTAATCT 539
DB 488 CCGCGAGCGGG-ANTTGTGTCGTCAGAGACTCCGGGAGCANTAGTCCGTAATCT 546
OY 540 CCGCGAGCGGAACCTAATTAACCCGTCNTCCAAANAAGTGGCCCTCTGGATCCCTT 599
DB 547 GCGCGGAGAACCTAATTAACCCGTCNTCC-ANGACGTGCCCCCTCTGGATACCTT 602
OY 600 TAAACNCAANTGAATCTCNCNTNANGAAGAACTCTTATGAACCTTAAACNA 659
DB 603 TAAACAGCAGCAATTAATACCTCC-AGGAAGAACTCTTATGAACNCTTAAACNA 660
OY 660 TCGATGAGACNCTGCTCTGTCACACATTTGCCAATGGCGCTGTCACACNCAATTTG 719
DB 661 TCGATGAGACCCG--TGTCACTTCACATTTGCCAATGGCGCTGTCACACATCAA-TTA 717
OY 720 NTCCCCAANTCTTCTCTCCTGCTCCCTCCCT--CCCAATGCAACCCCGGGAATTCCT 777
DB 718 ATCACCAACNTCATNTCCATGCTCCACACNTCCACAAATGCMACCCACACNCAATTCCT 777
OY 778 NTCCCCNCTCCCT 792
DB 778 TGTGCCACTCTCTT 792

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RESULT 5
AA69460
ID AA69460 standard; cDNA; 727 BP.
AC AA69460;
XX 15-MAR-1999 (first entry)
DT Banana fruit ripening-related clone U-139 cDNA.
DE Fruit ripening; banana; modulator; tissue senescence; crop; plant;
KM triploid; plant breeding; ss.
XX Musa acuminata.
XX WO9853085-A1.
PN 26-NOV-1998.
PD 05-MAY-1998; 98WO-GB01297.
PF 20-MAY-1997; 97GB-0010370.
XX (ZENB ) ZENECA LTD.
PI Bird CR, Medina-Suarez RDJ, Seymour GB;
XX WPI; 1999-059745/05.
DR New method of modulating fruit ripening or tissue senescence
PT characteristics of Musa plants - by introducing DNA sequences,
PT useful in processes for modifying plant/fruit ripening
PT characteristics
XX
PS Claim 1; Page 30-31; 78pp; English.
XX AA69440-V69512 are cDNA sequences which are used in a method to
CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC acuminata (banana) plants. The method provides a recombinant way of
CC modulating ripening/senescence characteristics of bananas, which are a
CC globally important crop. In particular, the method can modulate such
CC characteristics in the desert banana, which due to its triploid nature

```


CC is unaffected by conventional plant breeding techniques.

XX Sequence 727 BP; 144 A; 199 C; 202 G; 157 T; 25 other;

XX Query Match 71.0%; Score 572.2; DB 20; Length 727;

XX Best Local Similarity 90.9%; Pred. No. 2.4e-160;

XX Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

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QY 1 TGTTCCTCCTTCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAACGAGGCG 60
DB 16 TGTTCCTCCTTCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAACGAGGCG 75
QY 61 GCAATGACGGCGGTTTAAATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 76 GCAATGACGGCGGTTTAAATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
QY 121 CTGTTTGAACGAGGCTGGGGGATGATGGAAGCGAGAGTCTCTGCTGCAAGAT 180
DB 136 CTGTTTGAACGAGGCTGGGGGATGATGGAAGCGAGAGTCTCTGCTGCAAGAT 195
QY 181 GCGGAGCATCGCGAGAGCTTGAAGAGAGCTCCGGAACGGAGCGCGATGCT 240
DB 196 GCGGAGCATCGCGAGAGCTTGAAGAGAGCTCCGGAACGGAGCGCGATGCT 255
QY 241 TCTTTGAAGAGAGGCTGTAACTCCGGGACAGAGCCGAGTGCAGCAGCGAGAG 300
DB 256 TCTTTGAAGAGAGGCTGTAACTCCGGGACAGAGCCGAGTGCAGCAGCGAGAG 315
QY 301 GTTCTTCGACGGCTCTGATGATCAATTAACAGCAGCGCTGCGAGATCTTGGTAT 360
DB 316 GTTCTTCGACGGCTCTGATGATCAATTAACAGCAGCGCTGCGAGATCTTGGTAT 375
QY 361 CTGTCGTGCGGTTGAGGACACCGCATGACAGCTGTGGCGGGA-CCCTGATGGCA 419
DB 376 CTGTCGTGCGGTTGAGGACACCGCATGACAGCTGTGGCGGGA-CCCTGATGGCA 435
QY 420 TGTCAACAGAAAAAGCTCGCTGACTGGGCGATGGCTTTGAGGCAACGCAATGATG 479
DB 436 TGTCAACAGAAAAAGCTCGCTGACTGGGCGATGGCTTTGAGGCAACGCAATGATG 495
QY 480 CCGGAGCGGGGATTTGTTGTTGAGACAGCTCCGGGAGCAATGATCCCGTGATGCT 539
DB 496 CCGGAGCGGGGATTTGTTGTTGAGACAGCTCCGGGAGCAATGATCCCGTGATGCT 554
QY 540 CGCCCGGAGACATTANATACCCCGTCTCCCAANGAAGTTCGCCCTCTGGGATCCCTT 599
DB 555 CCGCCCGGAGACATTANATACCCCGTCTCCCAANGAAGTTCGCCCTCTGGGATCCCTT 610
QY 600 TAAACNCAATGGAATCTCNCNCAANGAAGAACTCTTATGAACAGCTTTAANCA 659
DB 611 TAAACNCAATGGAATCTCNCNCAANGAAGAACTCTTATGAACAGCTTTAANCA 669
QY 660 TCGATGACNCGTCTGCTGTCACATTTGCCAATGGGCGCTGCTGCAACCAAT 717
DB 670 TCGATGACNCGTCTGCTGTCACATTTGCCAATGGGCGCTGCTGCAACCAAT 726

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RESULT 6

AAV28658 ID AAV28658 standard; cDNA: 727 BP.

XX AAV28658;

XX 29-JUL-1998 (first entry)

XX Ripening banana pulp cDNA clone U-089 seq ID NO:16.

XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;

XX genetic control; tissue senescence; ss.

XX Musa acuminata.

XX W0811228-A2.

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XX 19-MAR-1998.
PD 08-SEP-1997; 97WO-GB02424.
XX 25-APR-1997; 97GB-0008366.
PR 10-SEP-1996; 96GB-0018862.
XX (ZENE) ZENECA LTD.
XX Bird CR, Medina-Suarez RDI, Seymour GB.
XX WPI: 1998-207389/18.
PR Modulation of ripening or tissue senescence in bananas - comprises
PR use of DNA isolated from ripening banana pulp to produce genetically
PR modified fruit
XX Claim 1: Page 28; 72pp; English.
XX The present sequence represents a cDNA clone isolated from ripening
CC banana pulp. 57 clones were isolated and are given in AAV28643 to
CC AAV28699. The cDNA clone sequences can be used in a method of modulating
CC ripening or tissue senescence process in plants of the genus Musa. The
CC method comprises: (a) inserting into the plant material at least 1 of the
CC 57 sequences (as above); (b) regenerating the plant material, and (c)
CC selecting from the transformed regenerants, plants with modulated
CC ripening or tissue senescence characteristics. Also described in the
CC present invention are: (1) plants, their progeny, seed and material
CC obtained from the plants, produced by the above method; (2) a vector
CC functional in plants comprising a promoter region which is operably in
CC plant cells, a polynucleotide sequence as defined above, and a
CC transcription termination sequence; and (3) a method of controlling
CC plant pathogens comprising the application of anti-pathogenic agent to
CC plants of (1).
SQ Sequence 727 BP; 145 A; 205 C; 196 G; 159 T; 22 other;
XX Query Match 67.5%; Score 543.8; DB 19; Length 727;
XX Best Local Similarity 86.6%; Pred. No. 7e-152;
XX Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;
QY 2 GTTCTCTCTTCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAACGAGGCGG 61
DB 8 GTTCTCTCTTCATCATCTTTTGTCTGTGGAAACGTGAGAGTGAACGAGGCGG 67
QY 62 CAATGAGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
DB 68 CAATGAGCGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
QY 122 TGTGTTTGAAGAGAGTGGGGGATGATGGAAGAGAGTCTCTGCTGCAAGATG 181
DB 128 TGTGTTTGAAGAGAGTGGGGGATGATGGAAGAGAGTCTCTGCTGCAAGATG 187
QY 182 GCGGAGCATCGCGGAGAGCTTTGAGAGAGCTCCCGGAACGCGACAGCGCGATGCTT 241
DB 188 GCGGAGCATCGCGGAGAGCTTTGAGAGAGCTCCCGGAACGCGACAGCGCGATGCTT 247
QY 242 CTTTGAAGAGAGGCTGTAACCCGGGAGAGAGAGCGAGTGCAGACACCCGAGGAGG 301
DB 248 CTTTGAAGAGAGGCTGTAACCAAGAGAGAGAGAGCGAGTGCAGATCTCTGTTATC 307
QY 302 TTGCTTCGACGGCTCTGATGACATTAATCAACAGACAGCGCTGCGAGATCTTGGTATC 361
DB 308 TTGCTTCGACGGCTCTGATGACATTAATCAACAGACAGCGCTGCGAGATCTTGGTATC 367
QY 362 TGTGTTGCTTCAGGCAACCCGATCGACAGCTGTGGCGGTGCGACCTTATGGCATG 421
DB 368 TGTGTTGCTTCAGGCAACCCGATCGACAGCTGTGGCGGTGCGACCTTATGGCATG 427
QY 422 TCAACGAAAAAAGCTGCTGACTGCGGATTTGGCTTTGG-ACGCAACGCAATGATG 480
DB 428 TCAACGAAAAAAGCTGCTGACTGCGGATTTGGCTTTGGCCCGCAACGCAATGATG 487

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PD 26-NOV-1998.
 XX 05-MAY-1998; 98WO-GB01297.
 XX 20-MAY-1997; 97GB-0010370.
 XX (ZENEC) ZENEC LTD.
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI: 1999-059745/05.
 DR
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX
 PS Claim 1; Page 22; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX
 SO Sequence 704 BP; 146 A; 190 C; 191 G; 149 T; 28 other;
 Query Match 63.4%; Score 510.8; DB 20; Length 704;
 Best Local Similarity 86.8%; Pred. No. 4.8e-142;
 Matches 603; Conservative 0; Mismatches 86; Indels 6; Gaps 5;
 QY 10 CTTCGATCAGATCTTTTGTCTGTGGAAAGCTGAGAGTGAGAGAGGCGGCAATGACG 69
 DB 5 CTTCGATCAGATCTTTTGTCTGTGGAAAGCTGAGAGTGAGAGAGGCGGCAATGACG 64
 QY 70 GCGGGTTTAAAGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 129
 DB 65 GCGGGTTTAAAGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
 QY 130 AAGGAGGTGGGGGGTGGATTTGGAAGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 189
 DB 125 AAGGAGGTGGGGGGTGGATTTGGAAGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 184
 QY 190 TCGGAGAGAGCTTTGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
 DB 185 TCGGAGAGAGCTTTGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 244
 QY 250 GAGAGGCTGTAACTCCGGGAGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309
 DB 245 GAGAGGCTGTAACTCCGGGAGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 304
 QY 310 ACGGTCCGATGACATTAATCAACAGAGCGGCTGGAGATCTCTCTCTCTCTCTCTCTCTCT 369
 DB 305 ACGGTCCGATGACATTAATCAACAGAGCGGCTGGAGATCTCTCTCTCTCTCTCTCTCTCT 364
 QY 370 GGTTCAGGCAACCGATGAGAGCTGTGGGCTGCGACCTGATTTGGCATGCAACAG- 428
 DB 365 GGTTCAGGCAACCGATGAGAGCTGTGGGCTGCGACCTGATTTGGCATGCAACAG- 424
 QY 429 AAAAAAGCTGCTGACTGCGGCAATTTGGTGAAGCAACGATNATNGTGGCCCGAGAG 488
 DB 425 AAAAAAGCTGCTGACTGCGGCAATTTGGTGAAGCAACGATNATNGTGGCCCGAGAG 484
 QY 489 GGAATTTGCTGCTGTGACAGAGCTCCGGGAGCATGATCCCGGATCTCTCTCTCTCTCTCT 548
 DB 485 GG-AMTGTACNTTGTACAGAGCTCCGGGAGCATGAT-CCCGGATCTCTCTCTCTCTCTCT 542
 QY 549 ACACTTANATAC-CCGCTCCTCCAGAGAGTGGCCCTCTGGATCCCTTTAAACN 607
 DB 543 ACACTTANATACNCCGCTCAGACCAAGAT--GCCCTCTGGGATCNCCTTTAAACCC 600

QY 608 AANTGGAATCTCNCCTCANGAGAACTCCTTTATGAACCTTTTAAACNATGATGGA 667
 DB 601 ACNTGGAATCTCNCCTCANGAGAACTCCTTTATGAACCTTTTAAACNATGGA 660
 QY 668 CACGATGCTCTCTGCTCAGATTTGCAATGCGGCTG 702
 DB 661 ATGACACNCCNGTTCACCTCAGCTTTCACATTTGCAATG 695
 RESULT 9
 ID AAV69458 standard; cDNA: 706 BP.
 XX AAV69458;
 AC
 XX
 AC
 XX
 DT 15-MAR-1999 (first entry)
 DE Banana fruit ripening-related clone U-114 cDNA.
 XX
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 OS Musa acuminata.
 PN W09853085-A1.
 XX
 PD 26-NOV-1998.
 PE 05-MAY-1998; 98WO-GB01297.
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENEC) ZENEC LTD.
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI: 1999-059745/05.
 DR
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX
 PS Claim 1; Page 29-30; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX
 SO Sequence 706 BP; 144 A; 192 C; 195 G; 153 T; 22 other;
 Query Match 61.6%; Score 496.8; DB 20; Length 706;
 Best Local Similarity 90.6%; Pred. No. 7.2e-138;
 Matches 639; Conservative 0; Mismatches 52; Indels 14; Gaps 10;
 QY 2 GTTCTCTCTGATGATCAATCTTTTGTCTGGAAGAGAGAGTGAAGAGAGGCGG 61
 DB 7 GTTCTCTCTGATGATCAATCTTTTGTCTGGAAGAGAGAGTGAAGAGAGGCGG 66
 QY 62 CAATGAGAGGCGGTTTAAATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
 DB 67 CAATGAGAGGCGGTTTAAATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
 QY 122 TGGTTTGAAGAGAGTCCGGGAGAGTGAAGAGAGAGTCTCTGCTCGAGAGATG 181
 DB 127 TGGTTTGAAGAGAGTCCGGGAGAGTGAAGAGAGAGTCTCTGCTCGAGAGATG 186
 QY 182 GCGGAGCATGCGGAGAGAGCTTGAAGAGAGCTTCCGGAACGAGCAGCGCATGCTT 241


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PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 11-AUG-1999; 99US-0148171.
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PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159350.
PR 14-OCT-1999; 99US-0159331.
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PR 14-OCT-1999; 99US-0159638.
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PR 21-OCT-1999; 99US-0160741.

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PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 21.0%; Score 169.4; DB 21; Length 1633;
 Best Local Similarity 63.5%; Pred. No. 4; 6e-40;
 Matches 304; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

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QY 274 GAGCCGAGTCGACGACCCGAGAGGTTGCTTCGACGGTCTGATGACCATATATAC 333
DB 243 GACATGACAGTTGAGAACCCAGATGAGTCGCTCCATGGTGACATGACATTCGAAAC 302
QY 334 AGCAGGCTGCGAGATCTGTTATCTGTCGCGCGGTTCAGGCAACCGATCGAGAC 393
DB 303 AGCAGAGAGCGGAGAGATTAAGTTACTTCTCTGCGCCACCGGCAACCCAAATCGAGAT 362
QY 394 TGTGCGGTCGCGACCCCTGATTTGCGATGTCACAGAAAAAGCTGCTGACTGGGCATT 453
DB 363 TGTGCGGTCGCGACCCCAATATGCGACCTCGTGGCAAGGTTAGCGATGCTCATATC 422
QY 454 GCGTTTGAGCAACGNNATNATGCGCGGAGCGGGAATTTGTTGTTGACAGATC 513
DB 423 GGATTTGCGCGAACGCAATCGAGCGCGGAC-GGTCTTTCTACGTCGTAACCGACCC 481
QY 514 CGGGAGNATGATCCCGTGATCCGCGCGGGAACACTTANATACCGCTGCTGCCAAN 573
DB 482 TGGAGAGGAGCAT-CCGCTTATATCCATACCGGAGACGTCGTCACGCGGTGATT- 537
QY 574 GAACTGCCCCCTGTGGATCCCTTTAAACNCAANTGAAATCTGCTNANGAGAGA 633
DB 538 -AAGAGAACCACTCTGATCATCTTCAAAACCGACATGGTTATAC-CTTGAAGCAAGA 595
QY 634 ACTGNTATGAACAGCTTTAAACNATGATGACGACNNGTGTCTGTCACATGGCAA 693
DB 596 GCTGATCATGAACGCTTCAAAACCATGATGTCGTGTCTCATATGTTACATCGCTAA 655
QY 694 TGGCGCTGCTGACCAACCAATTTGTCGCCAACNCTCTGTCNANGCTCNCNC 752
DB 656 TGGAGCTTGTCTCAAGTTACATGATGACATATTATGTCATGGATGATGTC 714

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RESULT 11
AAV69449 standard; cDNA; 823 BP.
AAV69449;
AC AAV69449;
XX 15-MAR-1999 (first entry)
XX
XX Banana fruit ripening-related clone U-51 cDNA.
DE
XX Fruit ripening; banana; modulator; tissue senescence; crop; plant;
KW triploid; plant breeding; ss.
XX
XX Musa acuminata.
OS
XX
XX W09853085-A1.
PN
XX

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PD 26-NOV-1998.
XX
XX 05-MAY-1998; 98WO-GB01297.
XX
XX 20-MAY-1997; 97GB-0010370.
XX
XX (ZENEC) ZENEC LTD.
XX
XX Bird CR, Medina-Suarez RDJ, Seymour GB;
XX
XX WPI; 1999-059745/05.
XX
XX New method of modulating fruit ripening or tissue senescence
XX PT characteristics of Musa plants - by introducing DNA sequences,
XX PT useful in processes for modifying plant/fruit ripening
XX PT characteristics
XX
XX Claim 1; Page 24; 78pp; English.
XX
XX AAV69440-V69512 are cDNA sequences which are used in a method to
XX CC modulate the fruit ripening or tissue senescence characteristics of Musa
XX CC acuminate (banana) plants. The method provides a recombinant way of
XX CC modulating ripening/senescence characteristics of bananas, which are a
XX CC globally important crop. In particular, the method can modulate such
XX CC characteristics in the desert banana, which due to its triploid nature
XX CC is unaffected by conventional plant breeding techniques.
XX
SQ Sequence 823 BP; 168 A; 266 C; 222 G; 150 T; 17 other;

Query Match 18 7%; Score 151; DB 20; Length 823;
Best Local Similarity 63.7%; Pred. No. 1,1e-34;
Matches 2/2; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

QY 327 AATCAACAGCAGCGCTCGCAGATCTTGTATCTGTCGCGTTACGACACCCGAT 386
DB 137 AAGCTTGAAGTGTGGCGGGCGGCGACTGGGCTACTTGTATCGGACCGGCAATCCAT 196
QY 387 CGACGACTGCTGCGGCTGCGACCTGATGGCATGTCAACAGAAAAGCTGCTGACTG 446
DB 197 CGACGACTGCTGCGGCTGCGATCTGACTGCGCCCAACCGCGACGCGCTGCGGACTG 256
QY 447 CGGCAATGGCTTGGACGACGCAATANGTGGCGCGCGGGAATTTGTTGTTGTA 506
DB 257 CGCCATCGGGTTCGGAGAGACGCAATGGGGGAGGAGCGCG-AGATATACGTGTA 315
QY 507 CAGACTCGGGGAGGACGATGCTCGGATCTCGCCCGGGAACACTTANATACCCGCTC 566
DB 316 CCGACAGTGGCGAGCAGCA-CCCGTCAATCCGAAGCGGGGAGCGTCCGATCCGCGTC 374
QY 567 ATCCAGNAGATGGCCCTCTGGGATCCCTTTAAACNCAANTGAAATCTCCTCNA 626
DB 375 ATCCAGGAGGAGCGCGCTGT---GGATCATCTTCAAGCGCGCATGTGTCATC-CAGTTGA 430
QY 627 NGAGAAGCTGTTATGAACAGCTTAAACNATGATGGAAGNCTGTCCTGCTCCACA 686
DB 431 AGGAGAGCTCATCTATGACTTCCACAGACCATGAGGCGGGGCGCAGCGTCCACA 490
QY 687 TTGCCAATGGCGCCCTGCTGCTACCAACCAATTTCTTCCCAACNTCTTCTCCNTGCTC 746
DB 491 TCTCGGGGGCGCGTGCATCAACCATCCAGTACGTCACCAACATATCATATCCAGGCGTC 550
QY 747 CNGTCCC 753
DB 551 CACATCC 557

XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 34171.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
XX
XX Protein identification; signal transduction pathway;
XX
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 200EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134370.
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XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.
XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
XX 18-JUN-1999; 99US-0139460.
XX 18-JUN-1999; 99US-0139461.
XX 18-JUN-1999; 99US-0139462.
XX 18-JUN-1999; 99US-0139463.
XX 18-JUN-1999; 99US-0139750.
XX 18-JUN-1999; 99US-0139763.

OY 574 GAAGTGGCCCTGCGGATCCCTTTAAACNMCNMTAGGAATCTCNCCTNANGAGAA 633
 DB 502 AA-----GAACCATTTAGTATGCTCTTTAAACGTGACATGTCATTAACA-TTAAAGANAGA 556
 OY 634 ACTCMTTNGACACCTTTAAANACNATGATGACNCGNCTGCTCCATATGGCCAA 693
 DB 557 ACTAATCATGAACAGTTTCAAAACATCGATGCTGCGGTCACAGTTTCAATAGCTTAA 616
 OY 694 TGGCGCTGCTCACCACCAATTTCTCCCAACNTCTTCTCCNTGCTCCNCTCC 753
 DB 617 TGGTCATGTATACAGATTCAGTGTGCTGACTTAACATTAATCATTCATTCAGGATTCATTTCA 676
 OY 754 CAAT 757
 DB 677 TGAT 680
 RESULT 13
 AAV69445
 ID AAV69445 standard; cDNA; 749 BP.
 AC AAV69445;
 XX 15-MAR-1999 (first entry)
 DE Banana fruit ripening-related clone U-11 cDNA.
 XX Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 XX Musa acuminata.
 OS W09853085-A1.
 XX 26-NOV-1998.
 PD 05-MAY-1998; 98WO-GB01297.
 XX 20-MAY-1997; 97GB-0010370.
 XX (ZENEC) ZENEC LTD.
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;
 PI WPI; 1999-059745/05.
 DR New method of modulating fruit ripening or tissue senescence
 XX characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 PT Claim 1; Page 21-22; 78pp; English.
 PS AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX Sequence 749 BP; 157 A; 245 C; 197 G; 128 T; 22 other:
 SO
 Query Match 17.9%; Score 144.4; DB 20; Length 749;
 Best Local Similarity 64.0%; Pred. No. 9.4e-33;
 Matches 275; Conservative 0; Mismatches 147; Indels 8; Gaps 5;
 OY 325 ATAATCAACAGCAGCGCTCGAGATCTCTGTTATCTGCTGCGGTTCAAGCAACCG 384
 DB 135 AGAAGCTTGAACGCTGCGGCGGCGGACTGCGCTTCTGATGCGGCGACCGCAATCG 194
 OY 385 ATCGACGCTGCTGCGGCTGCGGCGGCTGATTCGATTCACAGAAAAAGCTGCTGAC 444

DB 195 ATCGACGACTGCTGCGGCTGCGGCGGCTGACTGCGCTGACAAACCGGACGCGCTCGTAC 254
 OY 445 TCGGCATTTGGCTTGGAGCGCAACGCMATANGTGGCCCGGACGGGAATTTGCTGT 504
 DB 255 TCGGCATTTGGCTTGGAGAGAACGATGGGGCAGAGCGCG-AGATTAACNTGT 313
 OY 505 GACAGACTCCGGGAGCAATGATCCCGTGAATCTCGCCCGGGAACACTTAAATACCCG 564
 DB 314 GACCCAGAGTGGCGAGCAACNA-CCCCGTCATTCGAAAAACGGGACGGTCCGGTACGGCG 372
 OY 565 TCTTCCANGAAGTTGCCCGCTCTGCGGATCCCTTTAAACNMCNMTAGGAATCTCNCCT 624
 DB 373 TCATCC---AGAGAGACCCGCTGTGATCATCTTCAAGCGGACATGCTATCCAGCTG 428
 OY 625 NANGAGANA-CTCMTTATGAACAGCTTTAAANACNATGATGACNCGTGTCTGCTG 683
 DB 429 AAAGGAGAGAGCTCATCATGAACCTCCACACAGACCATGAGCGCGCGGCGGACGCTCC 488
 OY 684 ACATTGCCAATGCGCGCTGCTCACCACCAATTTCTCCCAACNTCTTCTCCNTG 743
 DB 489 ACATCTCCGGGCGCGGCGGCTGATCACCATCC-AGTAGCTACCAACATCATCCACGCG 547
 OY 744 CTCGCTGCC 753
 DB 548 GTCCACATCC 557
 RESULT 14
 AAV28659
 ID AAV28659 standard; cDNA; 842 BP.
 AC AAV28659;
 XX 29-JUL-1998 (first entry)
 DE Ripening banana pulp cDNA clone U-0115 SEQ ID NO:17.
 XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
 KW genetic control; tissue senescence; ss.
 XX Musa acuminata.
 OS W09811228-A2.
 XX 19-MAR-1998.
 PD 08-SEP-1997; 97WO-GB02424.
 XX 25-APR-1997; 97GB-0008366.
 PR 10-SEP-1996; 96GB-0018862.
 XX (ZENEC) ZENEC LTD.
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;
 PI WPI; 1998-207389/18.
 DR Modulation of ripening or tissue senescence in bananas - comprises
 XX use of DNA isolated from ripening banana pulp to produce genetically
 PT modified fruit
 PT Claim 1; Page 28-29; 72pp; English.
 PS The present sequence represents a cDNA clone isolated from ripening
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to
 CC AAV28659. The cDNA clone sequences can be used in a method of modulating
 CC ripening or tissue senescence processes in plants of the genus Musa. The
 CC method comprises: (a) inserting into the plant material at least 1 of the
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)
 CC selecting from the transformed regenerants, plants with modulated
 CC ripening or tissue senescence characteristics. Also described in the
 CC present invention are: (1) plants, their progeny, seed and material

CC obtained from the plants, produced by the above method; (2) a vector
CC functional in plants comprising a promoter region which is operably in
CC plant cells, a polynucleotide sequence as defined above, and a
CC transcription termination sequence; and (3) a method of controlling
CC plant pathogens comprising the application of anti-pathogenic agent to
CC plants of (1).

SQ Sequence 842 BP; 177 A; 277 C; 218 G; 154 T; 16 other;

Query Match	17.7%	Score 142.8	DB 19	Length 842
Best Local Similarity	64.3%	Pred. No. 3e-32		
Matches 276	Conservative 0	Mismatches 144	Indels 9	Gaps 5

QY	325	ATATATCAACAGCAGCGCTCGCAGATCTTGTGGTATATCGTGTGCGGTTACAGCAATCCG	384
Db	140	AGAACTTGAACGTGTGTCCGGCGCGGCGACTGGGCTTACTTGTATCGGCAACCGGCATCCG	199
QY	385	ATCGACGACTGCTGGCGGTGCGACCCCTGATTGGCATGTCAACAGAAAAAAGCTCGTGAC	444
Db	200	ATCGACGACTGCTGGCGGTGCGACCCCTGACTGGGTGTCAACACCGGCAAGCGGTCTGGTAC	259
QY	445	TGGCGATTGGCTTTGGACGCAAGCCNMTANGTGGCCGCGACGGGGAAATTTGTTGGTGT	504
Db	260	TGGCCATGGGTTGTGGGAAGACCGATTTGGGGCGAAGGACGGCG - AGATATACGGTGT	318
QY	505	GACGAGACTCGGGGGAACNTGATCCCCGGAATCTCGCCCGGGAACCTTANATATCCCG	564
Db	319	GACGCAAGATGGCGAAGNCGA - CCGCGTCANTCGAAAAACGGGACGACCTCGGTACCGCG	377
QY	565	TCATCCANGAAGTTGGCCCCCTCTGTGGATTCGCCCTTAAACNCAANTGAAATCTCCTC	624
Db	378	TCATTC - - - AGAGAGAGCCGCTGTGGATCATCTTCAAGCCGACATGCTATCCAACT -	432
QY	625	NANGAAGAAGTCNNTTATGAACAGTTTAAANCAANTGATGGAACNCGTGTCCGTCGA	684
Db	433	GAAGGAGGAGCTCATCATATGAACTCCCAAGACATGACGCGCCGGGCGCCACGGTCA	492
QY	685	CATTGGCAATGGCGCTCGTCACCAACCAATTTCTCCCAACNTCTTCTCCNTNGCC	744
Db	493	CATCTCCGGCGGGCCGTGATCACCAC - AGTAGGTACCAACATCATCATCCACGGCG	550
QY	745	TCCNCTCC	753
Db	551	TCCACATCC	559

RESULT 15

ID AAV69448 standard; cDNA; 708 bp.

AC AAV69448;

DT 15-MAR-1999 (first entry)

DE Banana fruit ripening-related clone U-31 cDNA.

FRUIT ripening; banana; modulator; tissue senescence; crop; plant;

3 XX

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DR WPI; 1999-059745/05.

PT New method of modulating fruit ripening or tissue senescence

PT useful in processes for modifying plant/fruit ripening

XX

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CC modulate the fruit ripening or tissue senescence characteristics of Musa

modulating ripening/senescence characteristics of bananas, which are a

CC characteristics in the dessert banana, which due to its triploid nature

XX
XX

COPYRIGHT

Best Local Similarity 60.38; Pred. No. 7.2e-32;
 Watchdog 300, Convergence 0, Watchdog 100, r=3.1e-3

[illegible]

50 Sequence 708 BP; 140 A; 225 C; 192 G; 134 T; 17 other;

Query Match	17.5%	Score 141.4	DB 20	Length 708
Best Local Similarity	60.3%	Pred No. 7.2e-32		
Matches 200; Conservative	0	Mismatches 182;	Indels 9;	Gaps 5

OY		325	ATATAAAGCAGCGGCTGGCAGATCTGTGGTTATCTGTGTGGTGAACCAACC	384
Dd		137	AGAACTTGAACTGTCCGGCGGCAGACTGGGCTACTTGTATGTGGGACCGGAATCCG	196
OY		385	ATCAGAGACTGCTGGCGGCTGCACCCGTATTGGCATGTCAACAGAAAAAACCTCGTGAC	444
Dd		197	ATCGAGAGACTGTGGCGGCTGCAGCCCTGACTGGCTGTACAACCGGACGGCTCGCGGAC	256
OY		445	TGGGCGATTGGCTTTGGAGCGCAACGCMNANTGTGCCCGCGACGGGGAAITTTGTCGTGT	504
Dd		257	TGGCGCTCGGTTCCGGGAAGACGGAGATTGGGGCGANGACGGCG--ANATATACGTGT	315
OY		505	GACAGACTCCGGGGAGCNATGATCCCCGTGAATCTCGCCCGGGAACATTANATACCCG	564
Dd		316	GACCGAAGTGGGAGCACMNA--CCCGTCATTCGAACCGGGGACGGTCCGGTAACCG	374
OY		565	TCNMCCANANAATTCCCCTCTGTGGATCCCCCTTAACMCNAMNTGGAAATCTCCTC	624
Dd		375	TCATCC---ANAGAAGCCGCTGTGGATCATCTTCAAAGCCGCAATGGTATCATCACTT	430
OY		625	NANGAAGAAGACTNTTATGACAGGTTTAAANCNATCATGAGCANCMNGTGTCTGCFA	684
Dd		431	AAGGAGGAGCTCATCTCNTGACTCCOACAAGACMTCAAGGGCGGGGGCGGCACAGTCCA	490
OY		685	CATTGCCAATGGSGCCTGCTGCTCACCANCAATTC-NTCCCAACNTCTTCTTCNTNGC	743
Dd		491	CATCTCCGGGGGCGCTGATCATTCAACCATCCAGTTACTTTCCNCAACATCATCTNTCCAGGC	550
OY		744	CTCCNC--TCCCAACAACCCNCCGGGAATTCCTNTGCCACNCTCCCTTCCTCATG	801
Dd		551	GTCACATTCACGACTGCAATCATCANGGGGGAACTCTCTNGTTGCGACCTCCCCCATNG	610
OY		802	G 802	
Dd		611	G 611	

Search completed: June 24, 2003, 00:50:33
Job time : 254 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 23:50:47 ; Search time 1449 Seconds
(without alignments)
9008.670 Million cell updates/sec

Title: us-09-966-881-13

Perfect score: 806
Sequence: 1 TGTCTCTCTCTGATGACCA.....TCCCTCTCTCTATGATNG 806

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pla:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	23.0	501	9	AI770665 606055G03
2	176	21.8	480	9	AJ469163 AJ469163
3	173.6	21.5	589	17	AZ135244 OSJNB011
4	170	21.1	595	14	BO741525 seq19e11
5	169.2	21.0	462	17	BH874844 bh874844
6	166	20.6	800	14	BQ999911 BQ999911

7	165	20.5	720	14	BQ870176	BQ870176	QGD8F08.y
8	164.4	20.4	784	17	AZ916009	AZ916009	Pat1_1.h1
9	162.4	20.1	685	14	BO795866	BO795866	EST 4804
10	150	18.6	632	13	BI959076	BI959076	HVSMER001
11	149.4	18.5	679	10	AV822011	AV822011	AV822011
12	149.2	18.5	883	10	BE035831	BE035831	MO10611.M
13	144.8	18.0	612	14	BO148154	BO148154	NE062C07F
14	143.8	17.8	420	14	BO134100	BO134100	san57c10.
15	141.2	17.5	518	14	BO104182	BO104182	fc2443.e
16	141	17.5	365	12	BF655654	BF655654	FWL 47.B1
17	140.2	17.4	634	10	AW223193	AW223193	EST300004
18	139.8	17.3	789	12	BG599600	BG599600	EST504495
19	138.8	17.2	341	10	AW398301	AW398301	EST298148
20	133.8	16.6	632	14	BO148911	BO148911	NE084D12F
21	130.4	16.2	541	10	AV527067	AV527067	AV527067
22	130.2	16.2	542	12	BG040772	BG040772	NXSI 114
23	130	16.1	629	10	AV827058	AV827058	AV827058
24	129.6	16.1	620	10	AV825500	AV825500	AV825500
25	126.6	15.7	539	10	AV527181	AV527181	AV527181
26	126.4	15.7	579	10	AV442702	AV442702	AV442702
27	126.4	15.7	727	14	BO634030	BO634030	NXRV063.H
28	125.8	15.6	362	10	AV420958	AV420958	AV420958
29	124.4	15.4	635	14	BO700242	BO700242	NXRV103.B
30	124.2	15.4	609	17	BH717800	BH717800	BOMER30TF
31	123.6	15.3	515	14	BO634633	BO634633	NXRV071.D
32	122.4	15.2	682	13	BI924648	BI924648	EST544537
33	122.4	15.2	686	14	BO401767	BO401767	CA_Bd004
34	122.4	15.2	876	16	BG441931	BG441931	CA_Ea001
35	121.4	15.1	764	17	BH838673	BH838673	BOHJ209TF
36	120.4	14.9	436	12	BG319625	BG319625	SD8B12.S0
37	120.2	14.9	786	17	BH647126	BH647126	BOMBBS2TF
38	119.4	14.8	605	12	BG045860	BG045860	aaa07c02.
39	117.4	14.6	666	12	BG599297	BG599297	EST504197
40	117.4	14.6	773	14	BO508106	BO508106	EST615521
41	116	14.4	728	14	BO699768	BO699768	NXRV128.F
42	115.4	14.3	473	13	BM492945	BM492945	NXRV_032
43	115	14.3	546	10	BF008833	BF008833	ss70a05.y
44	114.8	14.2	644	10	AW683073	AW683073	NF007A12L
45	114	14.1	567	13	BI471247	BI471247	sa895b04.

ALIGNMENTS

RESULT 1
LOCUS AI770665 501 bp mRNA linear EST 02-FEB-2000
DEFINITION 606055G03.x2 606 - Ear tissue cDNA library from Schmidt lab zea
Mays CDNA, mRNA sequence.

ACCESSION AI770665
VERSION AI770665.1 GI:5268701
KEYWORDS EST.
SOURCE zea mays.
ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 501)

AUTHORS Walbot,V
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606055 row: G column: 03.
Location/Qualifiers
1..501
/organism="Zea mays"

FEATURES
source

/cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt
 lab"
 /tissue_type="mixed"
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
 /lab_host="XLOLR (Stratagene)"
 /note="Organ: Immature ear; Vector: pBK-CMV; Site:1: EcorI
 ; Site:2: XhoI; Mixed ear tissue cDNA library from Schmidt
 lab"

BASE COUNT 111 a 178 c 137 g 75 t
 ORIGIN

Query Match 23.0%; Score 185; DB 9; Length 501;
 Best Local Similarity 69.2%; Pred. No. 8.7e-45;
 Matches 306; Conservative 0; Mismatches 128; Indels 8; Gaps 5;

QY 312 GGTCTGATGACATATCAACAGACGGCTGCGAGATCTGTGTTATCTGCTGGG 371
 DB 6 GCTCTGACAGTTCATCAACACATACAGCCCGCGAATCTGGGTACTCTGCGG 65
 QY 372 TTCAGCAACCCGATCGAGAGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 431
 DB 66 GACAGCAACCCCATCGAGAGCTGCGGCTGCGACCTGCGACCTGCGACAAACCGGAA 125
 QY 432 AAAGTCTGCTGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 491
 DB 126 GCGCTCTGCGGCTGCGGCTGCGGCTGCGACCTGCGACCTGCGACCTGCGAC 184
 QY 492 ATTTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 551
 DB 185 AGATCTAGTGTGCTACACACACCGAGAGTACGCA CCTGTACACCGCGCAAGGCGACC 243
 QY 244 CTCCCTGACGCGCTGATCCAGGAA---GAGCGCTGCTGATCATCTTCAACGGGACAT 299
 DB 612 GGAATCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 671
 QY 300 GGTCTGACAGCTC-AAGAGAGAGCTGATGTAAGAGCTTCAAGACATCGACGAGCGG 358
 DB 672 GTGTCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 731
 QY 359 GCGCAAGCTGACATCGCGCAATGCTGCTGATCATCATCC-AGTACATCATCAAGCTC 417
 QY 732 TTTCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 753
 DB 418 ATCATCCAGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 439

RESULT 2
 LOCUS AJ469163 480 bp mRNA linear EST 24-MAY-2002
 DEFINITION AJ469163 S00008 Hordeum vulgare cDNA clone S0000800244H10F1, mRNA
 sequence.
 ACCESSION AJ469163
 VERSION AJ469163.1 GI:21185119
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 480)
 AUTHORS Saven, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
 TITLE Barley EST's
 JOURNAL Unpublished (2002)
 COMMENT Contact: Schulman AH
 Institute of Biotechnology
 University of Helsinki
 P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
 Finland.

FEATURES Location/Qualifiers

source 1. .480
 /organism="Hordeum vulgare"
 /db_xref="taxon:4513"
 /clone="S0000800244H10F1"
 /clone_lib="S00008"
 /tissue_type="callus"
 /note="Callus K19"

BASE COUNT 102 a 175 c 134 g 69 t
 ORIGIN

Query Match 21.8%; Score 176; DB 9; Length 480;
 Best Local Similarity 68.2%; Pred. No. 4.5e-42;
 Matches 300; Conservative 0; Mismatches 132; Indels 8; Gaps 5;

QY 314 TCCGATGACATATCAACAGACGGCTGCGAGATCTGTGTTATCTGCTGGG 373
 DB 14 TCCGATGACATATCAACAGACGGCTGCGAGATCTGTGTTATCTGCTGGG 73
 QY 374 CAGGCAACCCGATCGAGAGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 433
 DB 74 CCGGCAACCCCATCGAGAGCTGCGGCTGCGACCTGCGACCTGCGACAAACCGGACG 133
 QY 434 AGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 493
 DB 134 GCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGACCTGCGACCTGCGACCTGCGAC 192
 QY 494 TTGTTCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 553
 DB 193 ATCTAGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 251
 QY 554 TAAATACCCGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCAT 613
 DB 252 GCGCTGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 307
 QY 614 AAATCTGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 673
 DB 308 TCAATACCTC-AGCAGAGAGCTCATCATGAAACATCTTCAAGACATGAGCGCGGCG 366
 QY 674 GTCTCTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCAT 733
 DB 367 GCCAAGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCAT 425
 QY 734 CTTCCTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCAT 753
 DB 426 CATCCAGCGGCTGCGGCTGCGGCTGCGGCTGCGACCTGATGGCATGCAAGAAA 445

RESULT 3
 LOCUS A2135244 589 bp DNA linear GSS 02-JUN-2000
 DEFINITION OSJNB0115A18r CUGI Rice BAC library (EcorI) Oryza sativa genomic
 clone OSJNB0115A18r, DNA sequence.
 ACCESSION A2135244
 VERSION A2135244.1 GI:8214537
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 589)
 AUTHORS Wing, R.A. and Dean, R.A.
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
 JOURNAL Unpublished (1998)
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seg primer: GGAAACAGCTATGACATG
 Class: BAC ends


```

Db      237  ACTTCTTTCATGCGGGGTCCGGGAACCCAAATCGAGACATGCTGGCGGTCCGAAACGCGT 296
QY      416  GGCATGTCAACGAAAAAAAGCTGCGTGACTGGGGATTTGGCTTTGGAGCCAAACGCAATAN 475
Db      237  GGTACGGCCCGCGCAAGCGCTTAGCAACTGGGCGATCGGTTTGGCGCAACGGCCATCG 356
QY      476  GTGGCCGGAGCGGGGAAATTTGTTCTGTTGACAGACATCCGGAGCAANATGATCCCGTGAA 535
Db      357  GGGCGCGGGAGC -GGCGCGTACTAGCTGCGTGGAGACCCGGGAGAGAGCA -CCAGTCAA 414
QY      536  TCTCTGCCCCGGGAGACATTANATACCCCGCTCMTCCANAGAGTTGCCCCCTCTGGGATCC 595
Db      415  CCGCAAAACCCGGCACCTCTCCGGCAAGCGGTGATCCAGGACCG - - - - -CCCCCTCTGGATCG 470
QY      596  CCTTTAAACNCNAATVGGAAATCTGCTGCTCNANAGAAAGAACTGTTATGAACAGCTTAN 655
Db      471  TGTTCACACCGGACATGTGTCATTAAC -CTTAAAGCAAGAACTCATATGATGAACGCTTCAAG 529
QY      656  ACNATCGATGAGCNCNCGTCTCTGCTGCACATTTGCCAATGGCGCTGCTGCACANCCAA 715
Db      530  ACCATCGAGAGCGCGCGGTGAAAGCTCACATCGCTTATVGGTGGCTGATCAACCATACAG 589
QY      716  TTT 717
Db      590  TTT 591

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RESULT 5	BH874844/c	LOCUS	DEFINITION
BH874844	hg22a06.b1	WGS-zmapF (JM107 adapted methyl filtered) Zea mays genomic clone hg22a06 5', DNA sequence.	462 bp DNA linear GSS 05-AUG-2001

KEYWORDS	GSS.
SOURCE	Zea mays.
ORGANISM	Zea mays

REFERENCE	1 (bases 1 to 462)
AUTHORS	Rabinowicz, P. D., O'Shaughnessy, A. L., Ballja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nasclmento, L., Zentavern, T., McComble, N. R. and Martensen, R. A.
TITLE	Genomic Shotgun Sequences from Zea mays (methyl-filtered)
JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McComble

FEATURES	Location/Qualifiers
source	1. .462

```

/clone.lib="MCS-xmasey" (JM107 adapted methyl filtered)"
/lab host="JM107 or DH5a"
/node="Organ: immature ears; Site:1: Xba I; Site:2: Xba I
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, and repeated, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
digested with 0.8 and 3 kb and were cloned into the vector
pXy reads in M13mp19. b/g reads in pUC19). The same

```

BASE COUNT	ligation was transformed in either JM107 or DH5a. "			
ORIGIN	59 a	150 c	159 g	94 t
Query Match	21.0%	Score 169.2	DB 17	Length 462
Best Local Similarity	69.5%	Pred No. 5.1e-40		
Matches 283	Conservative 0	Mismatches 116	Indels 8	Gaps 5

OY	647 AGCTTTAANACNATCGAGTCANGTGTCTCCGTCGCACATTGGCAATGGGCGCCTGCNTC	706
Db	169 AGCTTCAAGACCATTGAGCGGGGGGGGCCCAACGTCACATCGCCAAAGCGGGCGCTCGCTC	110
OY	707 ACCANCCAAITTCATTCGCCCAACGTCCTTTCTTCGATNAGCTCCNCNTCCC	753
Db	109 AACATTC-AGTAGCTGACCAACGTCATCATCCACAGGGGCTGCACATCC	64

RESULT 6					
BO999911					
LOCUS	BO999911	800 bp	mRNA	linear	EST 22-AUG-2002
DEFINITION	Q6G236308.yg.ab1 Q6_EFGHJ lettuce serritola				
	Q6G236308, mRNA sequence.				
ACCESSION	BO999911				
VERSION	BO999911				
KEYWORDS	BO999911.1 GI:22434307				
SOURCE	EST.				
ORGANISM	Lactuca sativa.				
	Lactuca sativa				

REFERENCE	1 (bases 1 to 800)
AUTHORS	Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison P., Koltman, J., Slabaugh, M. S., Livingston, K., Zhou, T., Daly, Z., Church, S., Jackson, L. and Bradford, K.
TITLE	Letuce and Sunflower ESTs from the Compositae Genome Project http://compomics.ucdavis.edu/
JOURNAL	Unpublished (2002)
COMMENT	Contact: Alexander Kozik [R.W.Michelmore]

```

FEATURES
SOURCE
Email: akozik@atgc.org [michalmore@vegnall.ucdavis.edu/
belongs to contig OG_CAContig5568, see http://cspdb.ucdavis.edu/
for details.
Plate: OG623
row: G column: 08.
Location/Qualifiers
1..800
/organism="Lactuca sativa"
/cultivar="L. serriola"

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/db_xref="taxon:4236"
/clone_11b="Q6-EFCHJ lettuce serriola"
/clone="Q6G23608"
/lab_host="E.coli"
/notes="vector: pRNCDSAF1AB: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpbd.ucdavis.edu/
TAG_SEQ=Not found"

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BASE COUNT ORIGIN	221 a	179 c	207 g	193 t
----------------------	-------	-------	-------	-------

Query Match	20.68;	Score 166;	DB 14;	Length 800;
Best Local Similarity	64.08;	Pred. No. 6.3e-39;		
Matches 297;	Conservative 0;	Mismatches 160;	Indels 7;	Gaps 4;

QY	274	GAACCCCAGTCGACGACCCCGAGAGGTTCTTCGAGCGTTCGATACCATTAATCAAC	333
Db	324	GAATAATGCTGTTCAGATCCCTGAGGAAGTGGTCTCCATGCGCTGAATATGTAATTAATAAC	383
QY	334	AGCAGCGCTGCAGATCTCTTGTTATCTGTGCTGCGGTTCAAGCCACCCGATGCAGAC	393
Db	384	AACACCCAAAGAAAMAAAACCTCGGATCTCTTCATGTGGAACCCGAAACCCCAATGCAGCAT	443
QY	394	TGCGAGGCGGTGCGACCCCGATTGGCATGTCAACGAAAAAAGATCGCTGATGGGGCAT	453
Db	444	TGCTGGGCTTCGACCCCAACTGGCAAAAAACCGAAACGCGCTCGCCGATGGGGCATC	503
QY	454	GGCTTTGGACGCAACGCNATANTGTGCGCGACGCGGGAATTTGTTCGTTGACAGACTC	513
Db	504	GGATTTGGCCCGAATGCAATCGAAGGTGCGAC--GGCGTTATTACATGTCACAGATTG	562
QY	514	CGGGGACNATATATCCCGTGAATCTGTGCGCCGGGAACTTAATATCCCGCTCNTCAAN	573
Db	563	CGGGGACGACAT--CCAGTGAACCCACGACCCGGCACCCCTCCGCGACCGCTCATTC---	618
QY	574	GAATTCGCCCCCTCTGGGATCCCTTTAAACNCNAAATGAAATCTCNCNTNANGAAGA	633
Db	619	-AAATATACCCCTCTTGGATGCTGTTCAAAGCGCATGATGAT--TCAATTGAAGCAAGA	676
QY	634	ACTCNTTATGAACAGCTTTTAAMACNATGATGAGCNCNGTGTCTCGTCACATTTGCCAA	693
Db	677	ACTATTATGAACAGTTTAAACACCATGATGTCGTGGAATCATATGTTCATATGGCGAA	736
QY	694	TGGGCGCTGCNTCAACNCAAAATTCNCCCAACNCTCTCTC	737
Db	737	TGGAGCTTGTAATTACTGGTCAATTTGCTACTAAATGTAATTAATCC	780

RESULT	7
B0870176	
LOCUS	B0870176
DEFINITION	B0870176 720 bp mRNA linear EST 15-AUG-2007
ACCESSION	OG8BF08.t9.abl OG_ABCD1 lettuce salinas Lactuca sativa cDNA clone
VERSION	B0870176
KEYWORDS	B0870176.1 GI:22256484
SOURCE	EST.
ORGANISM	Lactuca sativa.
	Lactuca sativa
	Lactuca sativa

REFERENCE
AUTHORS

1 (Pages 1 to 720)
Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,
Iln, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolman, J., Slabaugh, M. S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.

TITLE	lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL	http://compgenomics.ucdavis.edu/
COMMENT	Unpublished (2002)
	Contact: Alexander Kozlik [R.W.Mitchelmore]

Contact: Alexander Kozik (R.W. Michelmore)
Department of Vegetable Crops, R.W. Michelmore Lab
University of California at Davis (UCD)
Asmumson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@veggmail.ucdavis.edu]
belongs to contig OG_CA.Contig5568, see <http://cgpbdb.ucdavis.edu/>
for details.
Plate: QGD8 row: F column: 08.

FEATURES	Location/Qualifiers
source	1. .720

/organism="Lactuca sativa"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGDBF08"
 /clone_lib="QG-ABCDI lettuce salinas"
 /lab_host="E.coli"
 /note="Vector: pBRCNDNA51AB. The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cpbdb.ucdavis.edu/tag_lib-QG-ABCDI lettuce salinas
 TAG_TISSUE="shoots environmental stress"
 TAG_SEQ="TCGCACGGG"

BASE COUNT	201 a	156 c	186 g	177 t
ORIGIN				

Query Match	20.5%	Score 165;	DB 14;	Length 720;
Best Local Similarity	65.2%	Pred. No. 1.2e-38;		
Matches 290; Conservative	0;	Mismatches 148;	Indels 7;	Gaps 4

QY	27	GAAGCCGCAAGTGCAGACACCCCGAGGAGGTGGCTTGACGGTCCGATGACCATTAATCAAC	333
Db	226	GAAAAAGCGTTCAGATCTCTAGGAAGTGGCTCTCCATGGTTGAATGGTAATTAATAAACA	285
QY	334	AGCACGGCTGCAGATCTCTGGTTATCTGTGTGTCGGTTCCAGCAACCCGATGCAGAC	393
Db	286	AACACCGAAGAAAGAAAACCTCGATCTTCTCATGTGAAACCGGAAACCCAAATGAGCAT	345
QY	394	TGCTGGCGGTGGGACCCGATGGCATGTGCACAGAAAAGACGCGCTGACTGGGGATT	453
Db	346	TGCTGGCGGTGGACCCAACTGCGCAAAAAAACCGGAAACGCTGCGCATGTGGGATC	405
QY	454	GGCTTTGACGCAACGCNATANGTGGCCGCGACGGGGAAATTGTCTGTTGACAGATC	513
Db	406	GGATTTGGCGGAAATGCAATCGAGAGTGCAGAC -GGCGTTATTACATGATGCACAGATTC	466
QY	514	CGGGGACNATGATCCCCCGTGAATCTCTGCCCGGGGAAACTAANATACCCCGTCTCCAA	573
Db	465	CGGCGACGACGAT -CCAGTGAACCCACGACCCGGACCTCTCCGACGCGCTCAATT -	520
QY	574	GAAGTTGGCCCCCTGTGGGATCCCTTTAAACNCNANANGAAATCTCNCNTNANGAAGA	633
Db	521	-AAGATACCCCTTTGGATCGTGTTCAACGCCACATGGTGAT -TCAATTGAAGCAGA	578
QY	634	ACTCNTTATGAACAGCTTTAANANACATGATGACNCGTGTCTCGTCCACATTGGCAA	693
Db	579	ACTTATTATGAACAGTTTAAAAACCATGATGCTGTGAGATCAATGTTTATATCGGAA	638
QY	694	TGGCGCCTGCNTCACCANCAATTTT	718
Db	639	TGGAGCTTGTATTACTGTTCAATTT	663

RESULT	8
LOCUS	AZ916009 784 bp DNA linear GSS 15-MAR-2001
DEFINITION	PstI_1_h12-c-1_0 Maize PstI B73 Leaf Zea mays genomic, DNA sequence.
ACCESSION	AZ916009
VERSION	AZ916009.1 GI:13347280
KEYWORDS	GSS.
SOURCE	Zea mays.
ORGANISM	Zea mays.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 784)
TITLE	Missouri Maize Project--Maize Mapping Project.
JOURNAL	PstI Zea mays B73 PstI leaf tissue library unpublished (2001)
COMMENT	Contact: Schroeder S Missouri Maize Project--Maize Mapping Project University of Missouri 209 Curtis Hall, Columbia, MO 65211, USA Tel: 573 882 8214 Fax: 573 884 7850 Email: sschroeder@celephais.agron.missouri.edu Class: shotgun.
FEATURES	location/Qualifiers
source	1..784
	/organism="Zea mays"
	/cultivar="B73"
	/db_xref="taxon:4577"
	/clone_lib="Maize PstI B73 Leaf"
	/library_type="leaf"
	/lab_host="DHS alpha"
	/note="Organ: Leaf; Vector: pUC19; PstI digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to pUC19 transformed in DHS alpha
BASE COUNT	190 a 202 c 210 g 182 t
ORIGIN	
Query Match	20.4%; Score 164.4; DB 17; Length 784;
Best Local Similarity	70.0%; Pred. No. 1.9e-38;
Matches 266; Conservative 0; Mismatches 107; Indels 7; Gaps 4;	
OY	319 ATGACCAATTAACAAGCAGCGGGCCGACGATCTGTGTATTCGTCTGGCGTTACAGC 378
Db	412 AGGTGCATCAAGAACAAGCACGCCCGCGGAACCTCGGGTACTGTCTGGCGACAGC 471
OY	379 AACCCGATCGACGACTGCTGGCGTGCGACCCTGATTGGCATGTCAACAGAAAAAGCTC 438
Db	472 AACCAGATCGACGACTGCTGGCGTGCGACCTCGGACTCGGACTGCGACACGACAAACCGGACGGCTG 531
OY	439 GCTGACTGCGGCAATGGCTTTGAGCGCAACGCNMTANSTGGCCCGCGACGGGAAATTGTT 498
Db	532 GCCGACTGCGGCATCGGGTTGGCGCGCAACGCCAATCGCGCGCGCGAC -GCCAAGGTGA 590
OY	499 CGTGTGTGACAGATCCCGGGGACNMNTGCCCGGTAATCCCTCGGCCCGGGAACACTTAAT 558
Db	591 CGTGTGTGACGAGCCGAGCGACGACGANT -CCCGTGAACCCGCGGAGGAGCCCTCCGCG 649
OY	559 ACCCGCTCNMCCAANGAAGTTGGCCCCCTCTGGATCCCTTAACNCNMANTGGAATC 618
Db	650 ACGCCGTCATCC ----AGGAGGACCCGCTGTGGATCATCTTCAAACGGGACATGGTGATC 705
OY	619 TCNCTCANNGAAGACTCNTTATGAACAGCTTTAANANCNTGATGACNCNGTGTCT 678
Db	706 ACGGT -GAGGAGAGAGCTCATCAAGAACAGTTCAAGACATGACAGCGGCGGCCCA 764
OY	679 CGTCCACATTTGCCAATGGCG 698
Db	765 CGTGCACATGCGCAACGGCG 784

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
BQ795866	BQ795866	685 bp	mRNA	linear	EST 30-JUL-2002							
LOCUS	EST 4604 Ripening Grape berries Lambda Zap II Library Vitis											
DEFINITION	Vitis vinifera cDNA clone RT021D12 3', mRNA sequence.											
ACCESSION	BQ795866											
VERSION	BQ795866.1	GI:22010832										
KEYWORDS	EST											
SOURCE	Vitis vinifera.											
ORGANISM	Vitis vinifera.											
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.											
AUTHORS	1 (bases 1 to 685)											
TITLE	Abbal,P., Agasse,A., Ageorges,A., Anassova,R., Barrieu,F., Chouteau,C., Dedalichamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.											
JOURNAL	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages											
COMMENT	Unpublished (2002)											
FEATURES	Contact: Romieu C.											
SOURCE	Unité de Recherche des Produits de la Vigne											
	Institut National de la Recherche Agronomique											
	2, place Viala, 34 060 Montpellier Cedex 01, France											
	Tel: 00-33-(0)4-99-61-28-62											
	Fax: 00-33-(0)4-99-61-28-57											
	Email: romieu@ensam.inra.fr											
	Seq primer: 17.											
	Location/Qualifiers											
	1..685											
	/organism="Vitis vinifera"											
	/cultivar="Shiraz"											
	/db_xref="taxon:29760"											
	/clone="RT021D12"											
	/clone_id="Ripening Grape berries Lambda Zap II Library"											
	/dev_stage="ripening stage"											
	/note="Organ: Fruit; Vector: Lambda Zap II; Site.1: Eco RI											
	; Site.2: XhoI; Oriented library, construction described											
	in Generation of ESTs from grape berry (skin, pulp or											
	seeds) at various developmental stages by Terrier,N.,											
	Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158											
	(112): 1575-83 2001"											
BASE COUNT	171 a	166 c	180 g	168 t								
ORIGIN												
Query Match	20.1%	Score 162.4;	DB 14;	Length 685;								
Best Local Similarity	62.8%	Pred. No. 7.2e-38;										
Matches 297;	Conservative 0;	Mismatches 169;	Indels 7;	Gaps 4;								
QY	280	GCACTGCACGACCCCGAGAGAGCTGCTTCACAGCTCTCCTGACATGACCATATCAAGACAGC	339									
DB	206	GCACTTATATGACCCAGATGACAGTGGCTTCATGTGTGACATGACATGGAAAGACACA	265									
QY	340	GCTTCGACAGTCTCTGGTATATCTTCGTCGCGGTCAGCAACCCGATCGACAGCTCGG	399									
DB	266	GAGGAGAGGAATATAGTTATTTCTCTGCTGAGACTGTATCCCATTTGATG										


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BASE COUNT      184 a      182 c      137 g      176 t
ORIGIN
Query Match      18.5%; Score 149.4; DB 10; Length 679;
Best Local Similarity 65.3%; Pred. No. 6.3e-34;
Matches 269; Conservative 0; Mismatches 136; Indels 7; Gaps 4;

OY 274 GAAGCCGAGTGCAGACCCCGAGAGGTTGCTTCAGCGTCTGATGACCAATATCAGC 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 GAACATGACATGAGAACCCAGATGAGATGCTGCTGATGAGATGAGATGAGATGAGAC 334
OY 334 AGCAGCGCTGCAGATCTCTGTTATCTGCTGCGGTTCAGGCAACCCGATGAGAC 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 335 AGCAGAGACCGGAGATGAGATGAGTACTCTCTGCGGCAACCGGCAACCAATGACGAT 394
OY 394 TGTGCGGTGCGACCTGATGAGTGCATGACGAAAAAGCTGCTGATGCGGCAAT 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 395 TCTGCGGTGCGACCGCAAAATGCGAGCTGCTGCAAAAGCTTACCGATGCTGCAATC 454
OY 454 GCGTTGAGACGACGCAATGATGCGCGGAGGGAATTTGTTGCTGAGACAGAC 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 455 GATTTGCGCGGACCAATCGAGAGCGCGGAC -GCTGCTTCTGATGATGATGATGATG 513
OY 514 CGGGGACATGATCCCGGTGAATCTGCGCGGGAACCTTANATACCGCGTCTGTCAN 573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 514 TGGAGACGACGAT -CCCGTAAATCCCATACCGGGAACACTCGGTGACGCGATGATTC --- 569
OY 574 GAAGTTGCGGCTCTGAGGATCCCTTTAAACNCAANTGGAATCTCNCCTGACGAGA 633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 -AAGAGCAACCACTGATGATCATCTTCAACGCGATGATGATTAAC -CTTGAAGCAGA 627
OY 634 ACTGTTTGAACAGCTTAAACNATGATGAGACNCTGCTGCTGCTGCTGCTGCTGCTG 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 628 GTGATCATGATGACGCTTCAAAACCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679

RESULT 12
LOCUS      BE035831      883 bp      mRNA      linear      EST 07-JUN-2000
DEFINITION MO10G11 MO Mesembryanthemum crystallinum cDNA 5' similar to pectate
ACCESSION BE035831
VERSION BE035831.1 GI:8330840
KEYWORDS EST.
SOURCE common iceplant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 883)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
H., Kawaasak, S., McColough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chmeh@u.arizona.edu
An open reading frame exists.
Insert length: 2 Std Error: 0.00.
Location/Qualifiers
1..883
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="MO"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="5 weeks"

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BASE COUNT      217 a      201 c      221 g      241 t      3 others
ORIGIN
Query Match      18.5%; Score 149.2; DB 10; Length 883;
Best Local Similarity 61.0%; Pred. No. 8.3e-34;
Matches 289; Conservative 0; Mismatches 177; Indels 8; Gaps 4;

OY 280 GAGTGCAGACCCCGAGAGGTTGCTTCAGCGTCTGATGACCAATATCAGCAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 GCTGTGCTGACCCAGAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
OY 340 GCTGCAGATCTCTGTTATCTGCTGCGGTTCAGGCAACCCGATGAGACGATGCTG 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 CAGAGAGGAGAACCTGCTGATTTCTGATGAGACGGAATTCATGATGATGATGCTG 393
OY 400 CGGTGCGACCTGATGAGTGCATGACGAAAAAGCTGCTGATGCGGCAATGCTGCTT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 394 CGTTGATGCCAACGACGCAAAACCGCAAGCGCTGATGCTGATGCTGATGCTGCTT 453
OY 460 GACGCAACGCAATGATGCGCGGAGGGAATTTGTTGCTGACAGACTCCGCGGGA 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 454 GGAAGAAATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512
OY 520 CNAATGCTCCGCTGATCTGCGCGGGAACCTTANATACCGCGTCTGCTGCTGCTGCTG 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 513 TGAATGAT -GCTGCAACCTTAAAGCTGCGGCACTCTGCTGCTGCTGCTGCTGCTGCTG 567
OY 580 GCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 568 -GAGCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
OY 640 TATGAAACCTTAAACNATGATGAGACNCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 627 AATGAAACCTTCAAGACATGATGAGCGGCTGATGATGATGATGATGATGATGATGATG 686
OY 700 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 687 TTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 739

RESULT 13
LOCUS      B0148154      612 bp      mRNA      linear      EST 24-APR-2002
DEFINITION NF062C07FL1054 Developing flower Medicago truncatula cDNA clone
ACCESSION B0148154
VERSION B0148154
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1 (bases 1 to 612)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores-Jerez, I., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert length: 612 Std Error: 0.00
Plate: 062 row: C column: 07
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers
1..612

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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_1lb="NF06207FL"
/tissue_type="Developing flower"
/dev_stage="Developing flowers"
in early transition into pods."
very young, developing, fully-opened flowers and flowers
/enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using Exsist helper phage and the E. coli strain
XL1-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."
BASE COUNT      176 a      107 c      158 g      171 t
ORIGIN

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Query Match      18.0% Score 144.8; DB 14; Length 612;
Best Local Similarity 57.4%; Pred. No. 1.5e-32;
Matches 294; Conservative 0; Mismatches 211; Indels 7; Gaps 3;

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246 GGAAGAGAGGCTGTAAACCCGAGCAGAGAGCCGAGTGCAGACCCGAGAGAGTTGC 305
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
25 GGAAGAGAGGCTGTAAACCCGAGCAGAGAGCCGAGTGCAGACCCGAGAGAGTTGC 305
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
306 TTGACAGGCTCTTATGACCAATTAATCAACAGCAGAGCTCGCAGATCTTGTATCTGTC 365
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
85 TTCTAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 144
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
366 GTCCGCTTCCGAGCAGCCGATGAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 425
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
145 GTGTGAGAGCGGTAAACCCGAGCAGAGAGCCGAGTGCAGACCCGAGAGAGTTGC 204
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
426 CAGAGAGAGGCTGTAAACCCGAGCAGAGAGCCGAGTGCAGACCCGAGAGAGTTGC 485
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
205 CAGAGAGGCTGTAAACCCGAGCAGAGAGCCGAGTGCAGACCCGAGAGAGTTGC 264
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
486 CCGGAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 545
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
265 -TGGAAAGTACTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 322
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
546 GGAACACTTANATACCCGCTGCTGAGCAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 605
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
323 GGAACCTTTGGCGCAGCCGCTTATTCAGAGATAG-----ACCACCTTTGGATTTGTTCAAGA 377
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
606 CNAATGGAATCTCNCCTCNANGAGAGACTCTTATGAGACAGCTTATTAANACNATCGATG 665
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
378 GAGACATAGTTATGATTAAGAGAGCTTATGAGACAGTTCAAGACATATGATG 437
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
666 GACNCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
438 GAGAGAGAGTAAATGAGATATGCTAATGAGAGGTCATTAATCAATATGATGATGATGATGATG 497
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
726 AACCTCTTCCNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 757
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
498 ATGTTATCATTTCAATGCTTCAATATTCATGAT 529
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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RESULT 14
LOCUS      B0134100
DEFINITION B0134100 420 bp mRNA linear EST 19-Apr-2002
            sans/c10. y1 Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1052-3596 5' similar to TR:024416 024416 PEPTIDE LITASE. ; mRNA
            sequence.
ACCESSION  B0134100
VERSION    B0134100.1 GI:20208011
KEYWORDS   EST.
SOURCE     soybean.

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ORGANISM      Glycine max
REFERENCE     Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
              Glycine.
              1 (bases 1 to 420)
AUTHORS      Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
              A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
              Wyle, T., Underwood, R., Steptoe, M., Theising, B., Allen, J., Bowers
              Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
              R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
              R., Waterson, R. and Wilson, R.
              Public Soybean EST Project
              Unpublished (1999)
              Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available through: Resgen, Invitrogen Corp. 2130
              South Memorial Parkway Huntsville, AL 35801 For further information
              call: (800)-533-4363 or contact: cculresgen.com web site:
              www.resgen.com
              Seq primer: -40RP from gibco.
              Location/Qualifiers
              1. 420
              /organism="Glycine max"
              /db_xref="taxon:3847"
              /clone="SOYBEAN CLONE ID: Gm-c1052-3596"
              /clone_1lb="Gm-c1052"
              /tissue_type="whole seedlings of greenhouse grown plants"
              /dev_stage="1 week old"
              /lab_host="DH10B"
              /note="Vector: Bluescript II SK-. Site 1: EcoRI, Site 2:
              XhoI. The Harosoy N1L was constructed and seed was
              provided by Dr. J. Specht, University of Nebraska
              (Shoemaker and Specht, 1995). The cDNA library was
              constructed from mRNA isolated from whole seedlings of 1
              week old greenhouse grown plants. Complementary DNA was
              synthesized from mRNA using a primer consisting of a 3'
              poly(dT) sequence with a XhoI restriction site and a 3'
              anchor. EcoRI adapters were ligated to the blunt-ended
              cDNA fragments followed by XhoI digestion. The cDNA
              fragments were directionally cloned into the EcoRI-XhoI
              restriction site of the phuescript vector. The ligated
              cDNA fragments were transformed into DH10B host cells
              (GibcoBRL). The library was constructed in cooperation
              with Dr. Paul Keim's laboratory at Northern Arizona
              University."

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BASE COUNT      112 a      88 c      118 g      102 t
ORIGIN
Query Match      17.8% Score 143.8; DB 14; Length 420;
Best Local Similarity 63.2%; Pred. No. 2.4e-32;
Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;

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1 CCAAGAGAGAGTGTGCTGCTGAGAGGCTGTGAGACCATTAATCAAGCAGAGGAGAGAA 60
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351 TCTTGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
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61 GTTGGATTTTTCCTTGTGGAATGCAACCCCATATGATGATGCTGGGCTGCGAGCC 120
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411 TGATTTGCAATGTAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
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121 CAATGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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471 NATANGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 530
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181 CATCGGTGGCGGTGA -TGGAAATTTCTATGTGTGAGTGAACCCAGGAGGATGATGA -CCCT 238
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QY 531 GTGAATCTCTGCCCCGGGAACACTTANATACCCCGTCNTCCANGAAGTTGCCCCCTGTGG 590
DB 239 GTGAACCCGGAACCCGGCAGCTCTCGCCATGCTGTGATCC---AGGATTAACCATTTGG 294
QY 591 GATCCCTTTAANACNMANTGGAATCTCNCNTCANGAAGAAGTCTNTATGAACAGT 650
DB 235 GATTGTGTTCAGAGAGGAGCATGTTAT-TCAGCTGAACACAGAGCTGATCATGAACAGCT 353
QY 651 TTANACNATCGATGAGACNCGTGTCTCTGTCACATTCGCAATGAGCGGCTCCTCACC 710
DB 354 TCAAGACATGTGATGTAGAGAGATCAATGTCCACATTCCTAATGAGAGATCATCACA 413
QY 711 NCCATTT 717
DB 414 TTCAGTT 420

RESULT 15
BO104182
LOCUS fc2443.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
DEFINITION
Rosa hybrid cultivar cDNA clone fc2443.e 5', mRNA sequence.
ACCESSION
BO104182
VERSION
BO104182.1 GI:20153844
KEYWORDS
EST.
SOURCE
Rosa hybrid cultivar.
ORGANISM
Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosid I; Rosales; Rosaceae; Rosoideae; Rosa.
1 (bases 1 to 518)
Menda, N., Guterman, I., Plestun, D., Emanuel, M., Adam, Z., Pichersky
, E., Lewinsohn, E., Zamir, D., Vainshtein, A. and Weis, D.
Rosa petal genomics: an integrated approach to discover
fragrance-related genes
Unpublished (2002)
Contact: Naama Menda
Petal Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel
Tel: 972 8 9489 389
Fax: 972 8 9468 263
Email: shanama@rl.huji.ac.il
Seq primer: 73 forward.

FEATURES
Location/Qualifiers
source
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/organism="Rosa hybrid cultivar"
/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc2443.e"
/clone_1lb="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 134 a 129 c 147 g 108 t
ORIGIN
Query Match 17 5%; Score 141.2; DB 14; Length 518;
Best Local Similarity 63.1%; Pred. No. 1.7e-31;
Matches 268; Conservative 0; Mismatches 150; Indels 7; Gaps 4;
QY 274 GAAGCCGAGTCGACGACCCGAGAGGTTGCTTCAGCGTCCATGACCATATCAAC 333
DB 99 GAGCAGCGATGATTAATTCGAGAGATCCGCTCTGTTGATACGACCATTTGTAAC 158
QY 334 AGACGGGCTCGCAGATCTCTGTTATCTGTGTCGGGTTGAGCAACCGATCGACGAC 393
DB 159 AGTACTGCGAGAGAACTGGGATTTTTCATCGCGACAGAGGAATCCCATTCATGAC 218
QY 394 TGTGGGGGTGCGACCCCTGATTTGGCATGTCAACAGAAAAAGCTTGCTGACTGGCGATT 453

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DB 219 TCCTGGAGATGTGACCCACAAATGGCAGCCGCCACCCAGAGAGCTAGCCAACTGCGGCAAT 278
QY 454 GGCTTTGAGCGACGACNMANGTGGCCCGGAGGGGAATTTGTTGTTGACAGACTC 513
DB 279 GGGTTTGGCGGCAAGCGTCTCGCGGCGCTTGAC-GGAAGTACTACGTGTAAATGACCC 337
QY 514 CGGGGACNATGATCCCGGTGAATCTCGCCCGGGAACACTTANATACCCCGTCNTCCAN 573
DB 338 CGGTGATGATGA-CCCGGTGAACCCCGGCGGTAACTCCGTACAGCGTGTATCCAGG 396
QY 574 GAAGTTGCCCCCTCTGGGATCCCTTTAANACNMANTGGAATCTCNCNTCANGAAGA 633
DB 397 ACAG---GCCTTTGTGATGTGTCAAGCGTGAACATGTGATCACA-TTGAACGACGA 451
QY 634 ACTCNTATGAACAGCTTTAANACNATCGATGAGACNCGTGTCTGTCACATTCGCA 693
DB 452 GCTTATATGAACAGACTTCAAGACCATTCAGACCTGTGTGAGTGTCCACATTGCTTA 511
QY 694 TGGCG 698
DB 512 TGGAG 516

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Search completed: June 24, 2003, 01:15:01
 Job time : 1456 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:40:52; Search time 68 Seconds
(without alignments)
3635.022 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTCTCTCCCTTCGATCACA.....TCCCTCTCTCATGATGATG 806

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.6	6.9	1170	3 US-08-467-023-94	Sequence 94, Appl
2	55.2	6.8	1337	3 US-08-467-023-96	Sequence 96, Appl
3	55.4	6.7	1278	3 US-08-467-023-96	Sequence 96, Appl
4	46.6	5.8	1328	1 US-08-290-448A-58	Sequence 58, Appl
5	46.6	5.8	1328	1 US-08-290-448A-58	Sequence 58, Appl
6	46.6	5.8	1328	1 US-08-175-069A-58	Sequence 58, Appl
7	46.6	5.8	1328	1 US-08-461-939B-58	Sequence 58, Appl
8	46.6	5.8	1328	4 US-08-464-000-58	Sequence 58, Appl
9	46.6	5.8	1349	1 US-08-280-448A-73	Sequence 73, Appl
10	46.6	5.8	1349	1 US-08-290-448A-73	Sequence 73, Appl
11	46.6	5.8	1349	1 US-08-175-069A-73	Sequence 73, Appl
12	46.6	5.8	1349	4 US-08-461-939B-73	Sequence 73, Appl
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14	46.6	5.7	7218	1 US-08-232-463-14	Sequence 14, Appl
15	43.8	5.4	1320	1 US-08-280-448A-75	Sequence 75, Appl
16	43.8	5.4	1320	1 US-08-290-448A-75	Sequence 75, Appl
17	43.8	5.4	1320	1 US-08-175-069A-75	Sequence 75, Appl
18	43.8	5.4	1320	4 US-08-461-939B-75	Sequence 75, Appl
19	43.8	5.4	1320	4 US-08-464-000-75	Sequence 75, Appl
20	41.8	5.2	1160	1 US-08-280-448A-77	Sequence 77, Appl
21	41.8	5.2	1160	1 US-08-290-448A-77	Sequence 77, Appl
22	41.8	5.2	1160	1 US-08-175-069A-77	Sequence 77, Appl
23	41.8	5.2	1160	4 US-08-461-939B-77	Sequence 77, Appl
24	41.8	5.2	1160	4 US-08-464-000-77	Sequence 77, Appl
25	38.8	4.8	1196	1 US-08-280-448A-71	Sequence 71, Appl
26	38.8	4.8	1196	1 US-08-290-448A-71	Sequence 71, Appl
27	38.8	4.8	1196	1 US-08-175-069A-71	Sequence 71, Appl

28	38.8	4.8	1196	4 US-08-461-939B-71	Sequence 71, Appl
29	38.8	4.8	1196	4 US-08-464-000-71	Sequence 71, Appl
30	36.6	4.5	1036	4 US-09-072-596-304	Sequence 304, App
31	35.2	4.4	1368	1 US-08-290-448A-79	Sequence 79, Appl
32	35.2	4.4	1368	1 US-08-280-448A-79	Sequence 79, Appl
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34	35.2	4.4	1368	4 US-08-461-939B-79	Sequence 79, Appl
35	35.2	4.4	1368	4 US-08-464-000-79	Sequence 79, Appl
36	34	4.2	4403765	4 US-09-103-840A-2	Sequence 2, Appl1
37	34	4.2	4411529	4 US-09-103-840A-1	Sequence 1, Appl1
38	33.6	4.2	7218	1 US-08-232-463-14	Sequence 14, Appl
39	33	4.1	726	4 US-08-818-112-24	Sequence 24, Appl
40	33	4.1	726	4 US-08-818-111-24	Sequence 24, Appl
41	33	4.1	726	4 US-09-056-556-24	Sequence 24, Appl
42	33	4.1	726	4 US-09-072-596-24	Sequence 24, Appl
43	33	4.1	33529	4 US-09-144-085-3	Sequence 3, Appl1
44	33	4.1	4403765	4 US-09-103-840A-2	Sequence 2, Appl1
45	33	4.1	4411529	4 US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-467-023-94
Sequence 94, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irvin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE: CDS
NAME/KEY: 26..1126
LOCATION: 26..1126
FEATURE: mat_peptide
NAME/KEY: 89..1126
LOCATION: 89..1126
US-08-467-023-94

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Best Local Similarity 62.5%; Pred. No. 2.7e-07;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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DB 73 TGTATCTTGTACTCTGATTAATCCATCCACAGCTGCTGAGAGGATTCGAACCTGGCA 132
QY 420 TCTCAACAGAAAAAGCTGCTGACTGCTGCGGCAATGGCTTTGGACGCAACGNNATANGTG 479
DB 133 TCMAAACAGATGMAAGCTGCGACACTGTCTGTGGGATTGGAACTCCACCACTGGGAGG 192
QY 480 CCGGACGGGGAATT 495
DB 193 CAAGGAGGAGATT 208

RESULT 2
US-08-467-023-1
Sequence 1, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Crypomeria japonica
FEATURE:
NAME/KEY: CDS
LOCATION: 66..1187
FEATURE: mat_peptide
NAME/KEY: 129..1187
LOCATION: 129..1187
US-08-467-023-1

Query Match 6.8%; Score 55.2; DB 3; Length 1337;
Best Local Similarity 51.7%; Pred. No. 3.8e-07;
Matches 181; Conservative 0; Mismatches 159; Indels 10; Gaps 3;

QY 349 TCTCTGTTATCTCTGCTGCGCTTACGACACCCGATCGACACTGCTGGGGTGGCAC 408
DB 102 TCTTTTGTATTTGATGATCTTCTTCTGTATATCCCATGACAGCTGCTGGAGAGAGAC 161
QY 409 CCTGATTTGCGATGTCACAGAAAAAGCTGCTGACTGGGCAATGGCTTTGGACGCAAC 468
DB 162 TCMAACTGGGCCCCAAATGATGATGAGCTCCGAGATTGTCAGTGGCTTGGAGACTCC 221
QY 469 GCNATANGTGCCGCGACGGGGAATTTGTTGCTGTGACAGACTCGGGGACMATGATCC 528
DB 222 ACCATGGGAGGAGGAGAGAG -ATCTTATACGGTCAAGACTCAGATGAGCA -CC 276
QY 529 CCGTGAATTCCTGCGGGAACACTTANATCCCGTCTCCAAAGAGTTGCCCTCT 588
DB 277 CTGTAAATCTGACACGAGACTGCGCTATGAGCAACCGAATAGGCCCTGTGGA 336
QY 589 GGGATCCCTTAAACNCAANTGAAATCTCTCNANGAAGAACTCNTATGAGACAG 648
DB 337 TAATTTGAGTGGAATATGAAATATGAAAGCTCAAAATGCTATATGAC -ATTGCTGG 391
QY 649 CTTTAAACNATGATGACACNCTGTCTCTCCACTGCAATGGCG 698
DB 392 GTATAAGACTTTGATGCGAGGGAGCAAGTTATATGCAATGGCG 441

RESULT 3
US-08-467-023-96
Sequence 96, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1145
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 99..1145
US-08-467-023-96

Query Match 6.7%; Score 54; DB 3; Length 1278;
Best Local Similarity 61.8%; Pred. No. 8.6e-07;
Matches 84; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 360 TCTTCGTCGCGTTCAGCAACCCGATCGACGACTGCTGGCGGTGCGACCTGATTTGCA 419
DB 83 TGTATCTGTGCTGCTATATATCCCATAGACGCTGCTGAGAGAGATTCGAACCTGGGG 142
QY 420 TGTCAACAGAAAAGCTCGCTGACTGCGGCGATTGGCTTGAGCAACGCMATANGTG 479
DB 143 TCAAAACAGATGAAGCTCGAGATTTGGCGCTGTGGATTGGAACTCCACCATGGAGG 202
QY 480 CCGCGACGGGGAATTT 495
DB 203 CAAGGAGAGATTTT 218

RESULT 4
US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTCAGCAACCCGATCGACGACTGCTGGCGGTGCGACCTGATTTGCA 424
DB 113 CATGTGAAGCACACACATTTATAGCAAGTCTGAGGTGCAAGCCGATGGCGATA 172
QY 425 ACAGAAAAAGCTGCTGACTGCGGCGATTGGCTTGAGCAACGCMATANGTGCGCGG 484
DB 173 ACCGACAAGCGTTGCGCGATTGTGCCAAGGTTTGGCAAGGAACCTACGCTGGAANAAC 232
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGGACNATGATCCCGGATTCCTCGCC 544
DB 233 ATGTGAT-----GTCACACGCTACACGATATAAGTATGATGTTGCAAAATCCA 285
QY 545 GGAACACTTANATACCCGCTGCTCCANGAAGTTGCCCTCTGGGATCCCTTTAAAC 604
DB 286 AAGAGAGCACACTCCGTTGCTGCTGCCAANAAGAGCCCTTGTGATCATTTTAA 345
QY 605 NCNANTGGAATCTCNCCTCANGAAGAACTCTTTATGAACACTTTAANACATGAT 664
DB 346 AGAATATGTTGATTCATTGTAATCAAGAGCTGTGTAACACGACGACCAAGACCATGAT 405
QY 665 GGACNCNGTGTCTGTCCACATTGCCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTATACATGCTTAACGCCG 439

RESULT 5
US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGCGGTTGAGCAACCCGATGACGACTGCTGGCGGCGACCTGTGGCATGTCA 424
DB 113 CATGTGACACACACATTAATAGACAGTGTGGAGGTGCAAGCGGCGGATA 172
QY 425 ACAGAAAAAGCTCGCTGACTCGGCGATTGGCTTGGACGCAACGCMATANGTGCCGCG 484
DB 173 ACCGACAAACGTTAGCCGATGTGGCCCAAGGTTTCCAAAGGAACCTACGGTGGAAAA 232
QY 485 ACGGGAAATTTGTTGCTGTGACAGACTCCGGGACNATGATCCCGGTGATCTCGCC 544
DB 233 ATGGTGAT-----GTCTACACGGTCAACAGTGAATGAATGATGTTCCTCAATCA 285
QY 545 GGGAACTTANATACCCCGTCNTCCANAGATGCCCCCTGTGGATCCCTTTAAAC 604
DB 286 AAGAAGGACACACTCCGTTGCTGTGCTGCCAAACAGGCCCTTGATCATTTTAA 345
QY 605 NCNANTGGAATCTCNCNCNANGAAGAACTTATGACAGCTTTAANACNATCGAT 664
DB 346 ACAAATATGATTCATTTCATTTGAATCAAGAGCTTGTCTGAACAGCAGCAAGCATCAT 405
QY 665 GGACNCGTGTCTGTCACATTCGCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTTAACATCGTTAACGCCG 439

RESULT 6
US-08-175-069A-58
Sequence 58, Application US/08175069A
Patent No. 5776761

GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorun
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-175-069A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGCGGTTGAGCAACCCGATGACGACTGCTGGCGGTCGACCCCTGATGGCATGTCA 424
DB 113 CATGTGACACACACATTAATAGACAGTGTGGAGGTGCAAGCGGCGGATA 172
QY 425 ACAGAAAAAGCTCGCTGACTCGGCGATTGGCTTGGACGCAACGCMATANGTGCCGCG 484
DB 173 ACCGACAAACGTTAGCCGATGTGGCCCAAGGTTTCCAAAGGAACCTACGGTGGAAAA 232
QY 485 ACGGGAAATTTGTTGCTGTGACAGACTCCGGGACNATGATCCCGGTGATCTCGCC 544
DB 233 ATGGTGAT-----GTCTACACGGTCAACAGTGAATGAATGATGTTCCTCAATCA 285
QY 545 GGGAACTTANATACCCCGTCNTCCANAGATGCCCCCTGTGGATCCCTTTAAAC 604
DB 286 AAGAAGGACACACTCCGTTGCTGTGCTGCCAAACAGGCCCTTGATCATTTTAA 345
QY 605 NCNANTGGAATCTCNCNCNANGAAGAACTTATGACAGCTTTAANACNATCGAT 664
DB 346 ACAAATATGATTCATTTCATTTGAATCAAGAGCTTGTCTGAACAGCAGCAAGCATCAT 405
QY 665 GGACNCGTGTCTGTCACATTCGCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTTAACATCGTTAACGCCG 439

RESULT 7
US-08-461-939B-58
Sequence 58, Application US/08461939B
Patent No. 6335019

GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorun
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
Protein Allergen Using Peptides Which Include A T Cell Epit
NUMBER OF SEQUENCES: 93

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHYE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/461,939B
;; FILING DATE:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/464,000
;; FILING DATE: 05-JUN-1995
;; APPLICATION NUMBER: US 08/290,448
;; FILING DATE: 15-AUG-1994
;; APPLICATION NUMBER: US 07/529,951
;; FILING DATE: 29-MAY-1990
;; APPLICATION NUMBER: US 07/325,365
;; FILING DATE: 17-MAR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amy E. Mandragouras
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: IMI-018CNDY
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1328 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1328
;; US-08-461-939B-58
;;
Query Match 5.8%; Score 46.6; DB 4; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;
;;
QY 365 CGTCCGTCAGGCAACCCGATGAGAGACTGCTGGGGGTGCGACCCCTGATGGCATGTCA 424
DB 113 CATGTAGACACACACATTATATAGACAAGTGTGGAGGTGCAAGCCGATGGCGAATA 172
QY 425 ACAGAAAAAGCTCGTGAAGTGGGATGGCTTGGAGCAACGCNATANTGCGCGC 484
DB 173 ACCGACAAGCGTATGCGGATGTGCCCAAGTTTTCAGAAAGGAACTACGATGGGAAAC 232
QY 485 ACGGGGAATTTGTTGCTGTGTGACAGACTCCGGGAGACNATGATCCCGTGAATCCTGCC 544
DB 233 ATGTGAT-----GTCTACAGGTACACAGTATGAAGATGATGATGTGCAAAATCCA 285
QY 545 GGGAAACTTANATACCCCGCTCCTCCANAGAACTTGGCCCTTGGGATCCCTTAAAC 604
DB 286 AAGAAGGACACACTCCGGTTTGTGCTGCCAAAGAGGCCCTTGTGATCATTTTAA 345
QY 605 NCNANTGAAATCTCNCNANGAAGAACTGNTATGTAACAGCTTTAANACNATCGAT 664
DB 346 AGAAATATGTTGATTTATTTGATCAAGAGCTTGTGTAAACAGCCAAAGACCATGAT 405
QY 665 GGACNCGTGTCTCTGTCACATTTGCCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTAAACATCGTTAAGCCG 439
RESULT 8

US-08-464-000-58
;; Sequence 58, Application US/08464000
;; Patent No. 6335020
;; GENERAL INFORMATION:
;; APPLICANT: Rogers, Bruce
;; APPLICANT: Klapper, David G.
;; APPLICANT: Ratner, Thorunn
;; APPLICANT: Kuo, Mei-Chang
;; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
;; NUMBER OF SEQUENCES: 93
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHYE & COCKFIELD, LLP
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,000
;; FILING DATE: 05-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/290,448
;; FILING DATE: 15-AUG-1994
;; APPLICATION NUMBER: US 07/529,951
;; FILING DATE: 29-MAY-1990
;; APPLICATION NUMBER: US 07/325,365
;; FILING DATE: 17-MAR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amy E. Mandragouras
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: IMI-018CN2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1328 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1328
;; US-08-464-000-58
;;
Query Match 5.8%; Score 46.6; DB 4; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;
;;
QY 365 CGTCCGTCAGGCAACCCGATGAGAGACTGCTGGGGGTGCGACCCCTGATGGCATGTCA 424
DB 113 CATGTAGACACACACATTATATAGACAAGTGTGGAGGTGCAAGCCGATGGCGAATA 172
QY 425 ACAGAAAAAGCTCGTGAAGTGGGATGGCTTGGAGCAACGCNATANTGCGCGC 484
DB 173 ACCGACAAGCGTATGCGGATGTGCCCAAGTTTTCAGAAAGGAACTACGATGGGAAAC 232
QY 485 ACGGGGAATTTGTTGCTGTGTGACAGACTCCGGGAGACNATGATCCCGTGAATCCTGCC 544
DB 233 ATGTGAT-----GTCTACAGGTACACAGTATGAAGATGATGATGTGCAAAATCCA 285
QY 545 GGGAAACTTANATACCCCGCTCCTCCANAGAACTTGGCCCTTGGGATCCCTTAAAC 604
DB 286 AAGAAGGACACACTCCGGTTTGTGCTGCCAAAGAGGCCCTTGTGATCATTTTAA 345
QY 605 NCNANTGAAATCTCNCNANGAAGAACTGNTATGTAACAGCTTTAANACNATCGAT 664

Db 346 AGAATATGTCATTCATTGCAATCAGACGCTTGCTGTAACAGCCGACAGACCATGCAT 405
Qy 665 GGACNCGTCCTCGTCCACATTCGCCATGCGC 698
Db 406 GGCCGAGGGGTGAAGTAAACATCGTTAACGCCG 439

RESULT 9
US-08-290-448A-73

; Sequence 73, Application US/08290448A
; Patent No. 5676954

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainer, Thorunn
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Allergenic Proteins From Rayweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1323

US-08-290-448A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

Qy 365 CGTCGGTTCAGGACCCGATCGACGCTGCGCGTGCACCTGATGGCATGTCA 424
Db 134 CATGTGAAGCACACAACTTATAGCAAGTCTGAGGTGCAAGCCGATGGCGAATA 193
Qy 425 ACAGAAAAAGCTGCTGACGCTGCGGCAATGGCTTTGACGCAACGCNATANGTCCGCCG 484
Db 194 ACCGACAGCGCTTAGCCGATTTGCCCAAGGTTTGCAGGAACTACGCTGAGAAAC 253
Qy 485 ACGGGAATTTGTTGTTGACAGACTCCGGGACNATATCCCGTGAATCTCGCC 544
Db 254 ATGTGAT-----GTCTACAGCGTCAACGATATAAAGTATGATGTTGCAAAATCA 306

Qy 545 GGAACACTTANATACCCCGTCNTCAANGAGTTGCCCTCTGGATCCCTTTAAAC 604
Db 307 AAAGAAGCACACCTCGGTTTGCTGCTGCCAAAACAGCCCTGTGATCATTTTAA 366
Qy 605 NCNAAATGGAATCTCNCNTCAANGAAGAACTCATTATGAACAGTTTAANCAATCAT 664
Db 367 AGAATATGTCATTCATTGCAATCAGACGCTTGCTGTAACAGGACAGACCATTCAT 426
Qy 665 GGACNCGTCCTCGTCCACATTCGCCATGCGC 698
Db 427 GGCCGAGGGGTGAAGTAAACATCGTTAACGCCG 460

RESULT 10
US-08-290-448A-73

; Sequence 73, Application US/08290448A
; Patent No. 5698204

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainer, Thorunn
APPLICANT: Kuo, Mel-chang

TITLE OF INVENTION: Allergenic Proteins From Rayweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1323

US-08-290-448A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

Qy 365 CGTCGGTTCAGGACCCGATCGACGCTGCGCGTGCACCTGATGGCATGTCA 424
Db 134 CATGTGAAGCACACAACTTATAGCAAGTCTGAGGTGCAAGCCGATGGCGAATA 193
Qy 425 ACAGAAAAAGCTGCTGACGCTGCGGCAATGGCTTTGACGCAACGCNATANGTCCGCCG 484
Db 254 ATGTGAT-----GTCTACAGCGTCAACGATATAAAGTATGATGTTGCAAAATCA 306

Db 194 ACCGACAGCGTTAGCCGATTGTCGCCAAGGTTTTGCAAAAGGAACCTACGGTGGAAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCANNATGATCCCGTGATCCTCGCCC 544
Db 254 ATGGTGAAT-----GCTACACGGTCAACAGATGATTAAGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATATACCCCGTCTGTCACANGAAGTTGCCCTCTGGAGATCCCTTTAAAC 604
Db 307 AAAGAAAGCACACACCTCCGTTTGGCTGCTGCCAAAACAGCCCTTGTGATCATTTTAA 366
QY 605 NCNANANGAATATCTCCTCNCNANGAGAACTCTTTTGAACACTTTANACNATGAT 664
Db 367 AGAAATATGTTGATTCATTGGAATCAAGACTTGTGCTTAACACGACGACAGACCATCAT 426
QY 665 GGACNCNGTGTCTGTCACATTCGCAATGGCG 698
Db 427 GGCCGAGGGGTGAAGTTAATCATGTTAAGCCG 460

RESULT 11

US-08-175-069A-73
Sequence 73, Application US/08175069A
Patent No. 5776761

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-175-069A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTAGGCAACCCGATCGACAGCTGCGCGGTGGAGACCTGATTTGCATGTCA 424
Db 134 CATGTGAAGCAGACACATATTATAGCAAGTGCTGGAGTGGCAAGCCGATGGCGATA 193
QY 425 ACAGAAAAAAGCTGCTGACTGCGGGCATTTGGCTTTGAGACGACGANNATANGTGGCCG 484
Db 194 ACCGACAAAGGTTGCGGATTTGTCGCCAAGGTTTTGCAAAAGGAACCTACGGTGGAAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCANNATGATCCCGTGATCCTCGCCC 544
Db 254 ATGGTGAAT-----GCTACACGGTCAACAGATGATTAAGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATATACCCCGTCTGTCACANGAAGTTGCCCTCTGGAGATCCCTTTAAAC 604
Db 307 AAAGAAAGCACACCTCCGTTTGGCTGCTGCCAAAACAGCCCTTGTGATCATTTTAA 366
QY 605 NCNANANGAATATCTCCTCNCNANGAAGAACTCTTTTGAACACTTTANACNATGAT 664
Db 367 AGAAATATGTTGATTCATTGGAATCAAGACTTGTGCTTAACACGACGACAGACCATCAT 426
QY 665 GGACNCNGTGTCTGTCACATTCGCAATGGCG 698
Db 427 GGCCGAGGGGTGAAGTTAATCATGTTAAGCCG 460

RESULT 12

US-08-461-939B-73
Sequence 73, Application US/08461939B
Patent No. 6335019

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 03-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-461-939B-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGGCAACCCGATCGACGACTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAACACACACACATTATAGACAACTGCTGGAGGTGCAAGCCGATGGCGCAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTCGGCATTTGGTGGACGCAACGCNATANGTGGCCGCG 484
DB 194 ACCGACAAAGCGTTAGCCGATTTGTCGCCAAGGTTTTCAGAAAGGAACCTAGCGTGGAAC 253
QY 485 ACGGGAAATTTGCTGTTGTGACAGACTCCGGGACNATGATCCCGTGAATCTGCGCC 544
DB 254 ATGGTGAT-----GTCTACACGGTCAACAGTGAATGATGATGTTGCAATCCA 306
QY 545 GGAACACTTANATACCCCGTCCNTCCANAGATTGCCCTCTGGGATCCCTTAAAC 604
DB 307 AAAGAAAGCACACTCCGGTTTCTGCTGCCCAAAACAGGCCCTTGATGATCTTTTAA 366
QY 605 NCNAAATGGAATCTCNCNANGAAGAACTCTTATGACAGCTTTAANACNATCAT 664
DB 367 ACAAATATGATGATTCATTGTAATCAAGAGCTTGCTGAACAGGACAGCAAGCAATCAT 426
QY 665 GGACNCGTGTCTCTGTCACACTTGCACATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAACAATCGTTAACGCCG 460

RESULT 13
US-08-464-000-73

; Sequence 73, Application US/08464000
; Patent No. 6335020

; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mel-chang
; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,000
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,448
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: 29-MAY-1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: 17-MAR-1989

; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IM1-018CN2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-464-000-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGGCAACCCGATCGACGACTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAACACACACATTATAGACAACTGCTGGAGGTGCAAGCCGATGGCGCAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTCGGCATTTGGTGGACGCAACGCNATANGTGGCCGCG 484
DB 194 ACCGACAAAGCGTTAGCCGATTTGTCGCCAAGGTTTTCAGAAAGGAACCTAGCGTGGAAC 253
QY 485 ACGGGAAATTTGCTGTTGTGACAGACTCCGGGACNATGATCCCGTGAATCTGCGCC 544
DB 254 ATGGTGAT-----GTCTACACGGTCAACAGTGAATGATGATGTTGCAATCCA 306
QY 545 GGAACACTTANATACCCCGTCCNTCCANAGATTGCCCTCTGGGATCCCTTAAAC 604
DB 307 AAAGAAAGCACACTCCGGTTTCTGCTGCCCAAAACAGGCCCTTGATGATCTTTTAA 366
QY 605 NCNAAATGGAATCTCNCNANGAAGAACTCTTATGACAGCTTTAANACNATCAT 664
DB 367 ACAAATATGATGATTCATTGTAATCAAGAGCTTGCTGAACAGGACAGCAAGCAATCAT 426
QY 665 GGACNCGTGTCTCTGTCACACTTGCACATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAACAATCGTTAACGCCG 460

RESULT 14
US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367

; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:46:15 ; Search time 166 Seconds
(without alignments)
7124.978 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 1 TGTTCCTCCTTCGATCACA.....TCCCTTCCTCTATGATNG 806

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scoring table: 1042519 segs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	96.5	806	US-09-966-881-13	Sequence 13, Appl
2	543.8	67.5	727	US-09-966-881-16	Sequence 16, Appl
3	536	66.5	724	US-09-966-881-18	Sequence 18, Appl
4	142.8	17.7	842	US-09-966-881-17	Sequence 17, Appl
5	134.6	16.7	687	US-09-966-881-14	Sequence 14, Appl
6	124.2	15.4	1116	US-09-938-842A-1004	Sequence 1004, Ap
7	110.4	13.7	1215	US-09-938-842A-58	Sequence 58, Appl
8	93.4	11.6	460	US-09-770-444-439	Sequence 439, App
9	93	11.5	479	US-09-924-035A-174	Sequence 174, App
10	74.4	9.2	1629	US-09-938-842A-1766	Sequence 1766, Ap
11	68.4	8.5	277	US-09-923-876-4484	Sequence 4484, Ap
12	64.4	8.0	1185	US-09-938-842A-809	Sequence 809, App
13	56.2	7.0	388	US-09-878-574-3663	Sequence 3663, Ap
14	43.6	5.4	741	US-09-966-881-15	Sequence 15, Appl
15	41	5.1	1137	US-09-828-505-3	Sequence 3, Appl1
16	37.6	4.7	481	US-09-918-995-25	Sequence 25, Appl
17	37.4	4.6	708	US-10-123-155-298	Sequence 298, App
18	35.6	4.4	360	US-09-864-761-27334	Sequence 27334, A
19	35.6	4.4	496	US-09-864-761-10689	Sequence 10689, A

20	35.2	4.4	594	US-10-123-155-10	Sequence 10, Appl
21	35.2	4.4	15425	US-10-091-504-1654	Sequence 1654, Ap
22	35.2	4.4	15425	US-09-764-869-1654	Sequence 1654, Ap
23	34.8	4.3	451	US-10-123-155-126	Sequence 126, App
24	34.4	4.3	1732	US-09-789-561-21	Sequence 21, Appl
25	34.2	4.2	4100	US-09-373-658-29	Sequence 29, Appl
26	34	4.2	2396	US-10-098-841-96	Sequence 96, Appl
27	34	4.2	2663	US-10-098-841-97	Sequence 97, Appl
28	34	4.2	4332	US-09-764-891-5756	Sequence 5756, Ap
29	34	4.2	7149	US-10-166-935A-1	Sequence 1, Appl1
30	34	4.2	14155	US-10-108-605-102	Sequence 102, App
31	33.8	4.2	724	US-10-123-155-60	Sequence 60, Appl
32	33.8	4.2	1049	US-10-123-155-358	Sequence 358, App
33	33.4	4.1	437	US-09-960-352-12835	Sequence 12835, A
34	33.4	4.1	671	US-10-184-644-346	Sequence 346, App
35	33.4	4.1	671	US-10-184-634-346	Sequence 346, App
36	33.4	4.1	2380	US-09-964-992A-4	Sequence 4, Appl1
37	33.2	4.1	407	US-09-878-574-4048	Sequence 4048, Ap
38	33	4.1	519	US-10-123-155-210	Sequence 210, App
39	32.8	4.1	638	US-10-013-173-1	Sequence 1, Appl1
40	32.8	4.1	638	US-10-150-762-1	Sequence 1, Appl1
41	32.8	4.1	661	US-10-121-988-34	Sequence 34, Appl
42	32.8	4.1	661	US-09-884-998-34	Sequence 34, Appl
43	32.8	4.1	1064	US-09-804-682-29	Sequence 29, Appl
44	32.8	4.1	2481	US-10-121-988-35	Sequence 35, Appl
45	32.8	4.1	2481	US-09-894-998-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-966-881-13
Sequence 13, Application US/09966881
Patent No. US20020120960A1
GENERAL INFORMATION:
APPLICANT: Seymour, Graham
Bird, Colin
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19650
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966, 881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242, 860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-Sep-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-Sep-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Iiza D.
REGISTRATION NUMBER: 33, 712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 806 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: U-068
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-966-881-13

Query Match 96.5%; Score 778; DB 10; Length 806;
 Best Local Similarity 100.0%; Fred. No. 1.7e-244;
 Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TGTTCCTCTTCGATACATCTTTTGTCTGGGAAACGTGAGAGTGAAGAGGGG 60
DB 1 TGTTCCTCTTCGATACATCTTTTGTCTGGGAAACGTGAGAGTGAAGAGGGG 60
QY 61 GCAATGACGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 GCAATGACGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CTGGTTTGAAGGAGTGGGGGAGATTTGAAGGAGAGTCCCTCTGCTCGAGAT 180
DB 121 CTGGTTTGAAGGAGTGGGGGAGATTTGAAGGAGAGTCCCTCTGCTCGAGAT 180
QY 181 GCGGAGATCCGCGGAGAGTGTGAGAGAGGCTCCGCAACGCGACGCGGATGCT 240
DB 181 GCGGAGATCCGCGGAGAGTGTGAGAGAGGCTCCGCAACGCGACGCGGATGCT 240
QY 241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAGCCGAGTGAAGAGAGAG 300
DB 241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAGCCGAGTGAAGAGAGAG 300
QY 301 GTTGTGAGAGGCTGCTGATGACATTAATCAACAGAGAGGCTCGAGATCTCT 360
DB 301 GTTGTGAGAGGCTGCTGATGACATTAATCAACAGAGAGGCTCGAGATCTCT 360
QY 361 CTGTGCTGCGGTTTCAAGGACCCGATCGAGAGTGTGCGAGTGGACCTGAT 420
DB 361 CTGTGCTGCGGTTTCAAGGACCCGATCGAGAGTGTGCGAGTGGACCTGAT 420
QY 421 GTCAACAGAAAAAAGCTGCTGACCTGCGGATTTGGACGCAACCCNATANGTGC 480
DB 421 GTCAACAGAAAAAAGCTGCTGACCTGCGGATTTGGACGCAACCCNATANGTGC 480
QY 481 GCGGAGGGGAGATTGTCTGTGTGACAGATCCGGGGACNATGATCCCGTGAATCTC 540
DB 481 GCGGAGGGGAGATTGTCTGTGTGACAGATCCGGGGACNATGATCCCGTGAATCTC 540
QY 541 GCCCGGGAACCTTANATACCCGCTCCTCCCAANGAAGTTGCCCTCTGGGATCCCTTT 600
DB 541 GCCCGGGAACCTTANATACCCGCTCCTCCCAANGAAGTTGCCCTCTGGGATCCCTTT 600
QY 601 AAACNCAANTGGAATCTCNCNCTCNANGAAGAGACTCTTANGAACAGCTTTAANCAAT 660
DB 601 AAACNCAANTGGAATCTCNCNCTCNANGAAGAGACTCTTANGAACAGCTTTAANCAAT 660
QY 661 GATGAGACNNGTGTCTGTGACATTCGCAATGGCGCTGCTCCTCAGCANTTCN 720
DB 661 GATGAGACNNGTGTCTGTGACATTCGCAATGGCGCTGCTCCTCAGCANTTCN 720
QY 721 TCCCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
DB 721 TCCCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 781 CCCNCCTCCCTCTCTCTATGATNG 806
DB 781 CCCNCCTCCCTCTCTCTATGATNG 806

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RESULT 2

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US-09-966-881-16
; Sequence 16, Application US/09966881
; Patent No. US20020120960A1
; GENERAL INFORMATION:
; APPLICANT: Seymour, Graham
; Bird, Colin
; Medina-Suarez, Rosybel
; TITLE OF INVENTION: Genetic control of Fruit Ripening
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Zeneca Ag Products Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,881
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,860
; FILING DATE: 29-Mar-1999
; APPLICATION NUMBER: GB 9618862.8
; FILING DATE: 10-Sep-1996
; APPLICATION NUMBER: GB 9708366.1
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: PCT/GB97/02424
; FILING DATE: 08-Sep-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschultz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: SEE 50183/DST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: U-068
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
; US-09-966-881-16

Query Match 67.5%; Score 543.8; DB 10; Length 727;
Best Local Similarity 86.6%; Fred. No. 8.2e-168;
Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 2 GTTCTCTCTCTGATACATCTTTTGTCTGTGGAACGTGAGAGTGAAGAGGGG 61
DB 8 GTTCTCTCTCTGATACATCTTTTGTCTGTGGAACGTGAGAGTGAAGAGGGG 67
QY 62 CAATGACGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCT 121
DB 68 CAATGACGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCT 127
QY 122 TGGTTTGAAGGAGTGGGGGAGATTTGAAGGAGAGTCCCTCTGCTCTGAGATG 181
DB 128 TGGTTTGAAGGAGTGGGGGAGATTTGAAGGAGAGTCCCTCTGCTCTGAGATG 187
QY 182 GCGGAGATCCGCGGAGAGCTTGAAGAGAGCTCCGCAACGAGACGAGCCGATGCTT 241
DB 188 GCGGAGATCCGCGGAGAGCTTGAAGAGAGCTCCGCAACGAGACGAGCCGATGCTT 247
QY 242 CCTTGAAGAGAGGCTGTAAACCGGGGAGAGAGCCGCACTGACAGACCCCGAGAGAG 301

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```

: GENERAL INFORMATION:
: APPLICANT: Seymour, Graham
: Bird, Collin
: Medina-Suarez, Rosybel
: TITLE OF INVENTION: Genetic control of Fruit Ripening
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zeneca Ag Products Inc.
: STREET: 1800 Concord Pike
: CITY: Wilmington
: STATE: DE
: COUNTRY: USA
: ZIP: 19850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/966,881
: FILING DATE: 28-SEP-2001
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/242,860
: FILING DATE: 29-Mar-1999
: APPLICATION NUMBER: GB 9618862.8
: FILING DATE: 10-SEP-1996
: APPLICATION NUMBER: GB 9708366.1
: FILING DATE: 25-APR-1997
: APPLICATION NUMBER: PCT/GB97/02424
: FILING DATE: 08-SEP-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschultz, Liza D.
: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SEE 50183/UST
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (302) 886-1699
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 842 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: IMMEDIATE SOURCE:
: CLONE: U-0115
: SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-966-881-17

Query Match 17.7%; Score 142.8; DB 10; Length 842;
Best Local Similarity 64.3%; Pred. No.1.9e-36;
Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5

OY 325 ATAAATCAACAGCAGCGCTCGCAGATCTTGGTTATCTGTGCTGCGGTTACAGCAACCG 384
Db 140 AGAAGCTTGAACGCTGTCGCGGCGGCGAGATGGGCTCTTGTCTATGCGGCAACCGCAATCG 199
OY 385 ATCGACGACTCTGGCGGTGCGACCGCTATTGGCATGTCAACAGAAAAAGCTGCTGAC 444
Db 200 ATCGACGACTCTGGCGGTGCGACCGCTATTGGCATGTCAACAGAAAAAGCTGCTGAC 259
OY 445 TCGGCGATTTGGCTTGGACGCAACGCANATANGTGGCCCGACGCGGGAATTTGTCGTTGT 504
Db 260 TGGCGCATCGGGTTGCGGGAAGACGCATTTGGGCGGACGAGACGGCG -AGATTTACGTGT 318
OY 505 GACAGACTCGGGGACNATGATCCCGGTGAATCTCGCCCGGGAACACTTANATACCCG 564
Db 319 GACGACAGCTGTGGCGCNAAGA -CCCCCTCAATCCGAAAAACGGGACGCTCGCGTACCGG 377
OY 565 TCATTCGAANGAAGTTGGCCCTCTGCGGATGCCCTTTAAACNMANATGAATCTCNCCT 624
Db 378 TCATTC-----AGGAGAGACCGCTGTGATCATCTTCAACGCGGACATGATGATCAGCT- 432

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0Y      635 NANGAAGAAACCTTTATGACAAGCGTTTANANCMTGCATGGACNONGTCGTCCGA   684
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Db      433 GAGAGAAGAGCTCATCATBACTGCCCAACAAGCATTGCACGGCCGGGGCCCAAGCETCCA   492
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y      685 CATTGCCAATGGCGCGCTGCNTCACCANCCAATTTTCCCAACANTCTTCTTCNTNGCC   744
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
Db      493 CATCTCCGGCGGGCGCGTGATCACCAC--AGTAGGTACCAACATCATCATCAGCGGG   550
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
0Y      745 TCCNCTCCC   753
          ||| ||| |||
Db      551 TCACATCC   559

RESULT 5
US-09-966-881-14
; Sequence 14, Application US/09966881
; Patent No. US20020120960A1
; GENERAL INFORMATION:
; APPLICANT: Seymour, Graham
; Bird, Collin
; Medina-Suarez, Rosybel
TITLE OF INVENTION: Genetic control Of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: U-069
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-966-881-14

Query Match           16.7%; Score 134.6; DB 10; Length 687;
Best Local Similarity 61.6%; Pred.No.8..5e-34;
Matches 276; Conservative 0; Mismatches 163; Indels 9; Gaps 5
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OY      499  GGTGTGACACACACACCGGGGACNATGATCCCCGGATGCTCGCCCGGGAACTTANAT 558
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      180  CGTAGCTACTAGACCCACAGACGACAAT -CGGTTAACCTTAGACCCGGGACTTTACGTC 238
OY      559  ACCCGGTCNCCANAGAAAGTTGCCCCCTCTGGATGCCCTTTAAACNMCNANTGGAATC 618
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      239  ACCGCCGTGATCAAG-----ACGACACACTATGGATCGTTTCAAACGTGACATGATGAT 293
OY      619  TCNCTCNANAGSAAAGACTCNTTATGAACAGCTTTAAANACNATGATGGACNCGTGCCT 678
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      294  TCAGCTAAACAAAGAGCTATCGTTAACAGTTTAAACAGATCGATGAGAGCTGGCGCAA 353
OY      679  CGTCCACATTCGCCAATGGCGCCCTGTCNATCACCANCCAATTT 718
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      354  CGTTCACATTCCTAACGCTGGTGGTGCATTCACGATTCAGTTT 393

RESULT 7
US-09-938-842A-58
; Sequence 58, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE

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? CURRENT APPLICATION NUMBER: US/09/938, 842A
? CURRENT FILING DATE: 2001-08-24
? PRIOR APPLICATION NUMBER: US 60/227, 866
? PRIOR FILING DATE: 2000-08-24
? PRIOR APPLICATION NUMBER: US 60/264, 647
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/300, 111
? PRIOR FILING DATE: 2001-06-22
? NUMBER OF SEQ ID NOS: 5379
? SEQ ID NO 58
? LENGTH: 1215
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
US-09-938-842A-58

Query Match      13.7%; Score 110.4; DB 9; Length 1215;
Best Local Similarity 59.0%; Pred. No. 9,1e-26;
Matches 239; Conservative 0; Mismatches 159; Indels 7; Gaps 4;

OY 353 TTGGTATATCTGCTCGGGGTTACGAGCAACCGATCGACGACTGTGGCGGTGGACCTTG 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 TAGGTTACCTCTCATGTACGACGCGTAAACCAATCGACGACTGTGGCGTTGGACCTTC 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 413 ATTGGCATGTCAACGAAAAAAGCTCGCTGACTGCGGCAATTGGCTTTGGACGCAACGCA 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 ACTGTGGGCAACACCGTCAACGCTCCGCTGACTGCGCAATTGGATTGGCAAAAACGCCA 266

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Query Match	13.7%	Score 110.4	DB 9.4	Length 1215
Best Local Similarity	59.0%	Pred. No. 9.1e-26		
Matches	239	Conservative	0	Mismatches 159
				Indels 7
				Gaps 4
QY	353	TTGGTTAATCTGCTGTCGGTTTCAGGCAACCCGATCGAGACTGTCGGCGGTCCGACCTG	412	
Db	147	TAGGTACTCTCATGTACGACCGGTAAACCAATGAGACTGTTGGGGTGTGACCTC	206	
QY	413	ATTGGCATGTCAACAGAAAAAGCTCGCTGACTGCGGCAATTGGCTTTGGACGCAACGNA	472	
Db	207	ACTGGGACCAACACCGCTCAACGTCCTCGCTGACTGGCCATTGGATTGGCAAAAACGCCA	266	
QY	473	TANGTGGCGCGAGCGGGGAATTTGGTTGTGACAGACTCCGGGGAACNATGATCCCGGT	532	
Db	267	TCGGTGGCCGCTGAC-GGTGCGATTCTAGCTGGTGCACGACTCAGGAAAGA-CAACCCAGT	324	
QY	533	GAATTCCTCGCCGGGAACACTTANATACCCCGCTCTCCAAAGAAGTTGCCCCCTCTGGGA	592	
Db	325	TAGCCCCAAGCCCGGAACCTTTAAGACACGCGGTGGTCC-----AAGACAGCACCTCTGGA	380	
QY	593	TCGCCCTTTAAACNCNMAATGGAATCTCTNCTCNANGAGAAGCACTCTTATGAACAGCTTT	652	
Db	381	TCATCTTCCCAACGAGACATGACGATTCAGCTCAAA-GAAGAGCTATATCATGAACATATTC	439	
QY	653	AANCAATGATGAGACNCGTCTGCTCGCTGCACATTTGCATAGGGCGCTGNTCAACGNC	712	
Db	440	AAGACATCATGCGCCGTGGTGTCTTCGTCACACATCTTGGTGGCCCTTGATATACGATC	499	
QY	713	CAATTTCNCCCAACATCTTCTTCNCTNNGCCTCCNCTCCCAAT	757	

DB 500 CAGTACGACCAACATTAATCATTCATGGGATTCATATCCANGAT 544

RESULT 8

US-09-770-444-439
 ; Sequence 439, Application US/09770444
 ; Patent No. US2002023280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Mathew, Abraham V.
 ; APPLICANT: Ledford, Brookie L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Krieker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Allen, Keith R.
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurdan, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2027 (PARA-016PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,444
 ; PRIORITY FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,502
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 439
 ; LENGTH: 460
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(460)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-770-444-439

Query Match

Best Local Similarity 59.7%; Pred. No. 2.3e-20;
 Matches 182; Conservative 0; Mismatches 121; Indels 2; Gaps 2;

DB 268 GCAGCAGAAAGCCGACGACGACCCGAGAGGTTGCTTCGACGGTCTGATGACATTA 327
 DB 146 GCAGNNNGAATCCAGATGAGTACGAGAGGTTGCTTCGACGAGAAATGAGTGTG 205
 DB 328 ATCAACAGACGGCTGCGCATCTTGTGTTATGCTGTGCGGTTGACGACCAACCGATC 387
 DB 206 AAAAAACCATCCGAGAGGAGAACTAGTTACTTACTTGTGCGAAGCAAGCAAGCAAGCA 265
 DB 388 GACGACTGCTGGGCTGCGACCTGATGTCATGCAAGAAAAAGCTCGCTGACTGC 447
 DB 266 GACGATTTGTGGCGATGTGACCAATTTGGCAGCAAGAACCGTAAAGCGCTAGCGATTC 325
 DB 448 GGCATTTGCTTGAAGCAACCCATATGCTGCGCGGAGGAAATTTGTTGCTGTGAC 507
 DB 326 GGTATCGGATTTGAAGAAACGCAATCGGTGCTGATGAGAGCA-TTCTAGTAGTAC 384
 DB 508 AGACTCCGGGAGCAATGATCCCGTGAATCCTCGCCCGGAGCACTTAAATACCCGCTG 567
 DB 365 TGACCAAGAGACGACCAAT-NNGGTTAACCTAGACCGGGGACTTACGTACGCGCTGA 443
 DB 568 TCCAA 572
 DB 1111

DB 444 TCCAA 448

RESULT 9

US-09-924-035A-174
 ; Sequence 174, Application US/09924035A
 ; Patent No. US20020142319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2011US
 ; CURRENT APPLICATION NUMBER: US/09/924,035A
 ; PRIORITY FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: US 60/148,784
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 174
 ; LENGTH: 479
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(479)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-924-035A-174

Query Match

Best Local Similarity 61.0%; Pred. No. 3.1e-20;
 Matches 178; Conservative 0; Mismatches 112; Indels 2; Gaps 2;

DB 281 CAGTCGACGACCCCGAGAGGTTGCTTCGACGGTCTGATGACATTAATCAACAGCAG 340
 DB 178 CAGATGAGTAGGAGGAGCAAGTTCTGCTTGACAGAAATGAGTGAAGAAACCATACG 237
 DB 341 CTCGCAATCTGTGTTATGCTGTGCTGCGGTTGACGACCAACCGATGACAGTGTGC 400
 DB 238 AGAGGAGAACTAGGTTACTTACTTACTTCTGCGAAGCAAGCAAGCAAGTGTGTCG 297
 DB 401 GGTGCGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
 DB 298 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 357
 DB 461 GACGCAACCCATATGCTGCGCGGAGGAGGAAATTTGTTGTCAGACAGCTCGGAG 520
 DB 358 GAGAAACCGCATCGGTGCTGATGAGAGCA-TTCTAGTAGTACATGACCAAGAGAG 416
 DB 521 NATGATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
 DB 417 GACCAAT-NNGGTTAACCTAGACCGGGGACTTACGTACGCGCGTATCCAA 467
 DB 1111

RESULT 10
 US-09-938-842A-1766
 ; Sequence 1766, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIORITY FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22

QY 379 AACCCGATGGAGACACGTCGCGGGGGTGCGACCTGATTTGGCAGTGCACACAGAAAACATC 438
Db 139 AATCCGATGGACCTCGTGTGGCGGCTCAAGTCTGACTGGCTGCCAATCGTAAAGACCTA 198
QY 439 GCTGACATGGCGCATTTGGCTTTGGACGCAACGNCNATNANGTGCGCGGAGCGGGAATTTGTT 498
Db 199 GCGGATTTGCGTGGTTGGATTCCGTT-CATCTACCTTGGCGCGGAAGAAAGTTAATTATA 257
QY 499 CGTTGTGACAGACTCCGGGGACNATGATCCCGTGAACTCTGCGCCGGGAACACTTANAT 558
Db 258 CGTTGTGACAAACCTTTAGACAAATGACACA----GAATCTCAACACAGTCTTTGGCGT 313
QY 559 ACCCGCTCNTCCANAGAAAGTTGCCCCCTCTGGGATCCCTTTAAACNCAANTGGAATC 618
Db 314 ACGGCGTGAATCCAAAGCA----AACCATGTGATCACTTTCGGTAAAGATATGTCATA 369
QY 619 TCNCTCNANGAAGAACTCNTTATGACACGTTTAAACNATCGATGACACNCTGTCT 678
Db 370 ACCCTGAAAA-ATGACCTCATGTGTCATATGCTATTAACCACTTATGATGGAGAGGGCCAAA 428
QY 679 CGTCCACATTTGCCAATGGCGGCGCTGCTACCAACCA 715
Db 429 AGTAGAAATGCAATGCGACCATGATCACTCGATTCAA 465

